STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 176541

TO: Stephen Kapushoc Location: 3a60 / 2c70 Tuesday, January 17, 2006 Art Unit: 1634 Phone: 571-272-3312 Serial Number: 10 / 754446	From: Jan Delaval Location: Biotech-Chem Library Remsen 1a51 Phone: 571-272-2504 jan.delaval@uspto.gov

Search Notes

MG

176513

STIC-Biotech/ChemLib

From: Kapushoc, Stephen T.
Sent: Thursday, January 12, 2006 11:15 AM
To: STIC-Biotech/ChemLib
Subject: Sequence searches for 10/754,446

Please perform the following searches for application 10/754,446:

Score/Length sequence search for the following fragments of GenBank Locus AF287270, with a minimum hit length of 15 and a maximum hit length of 30, and a score over length cutoff at 90%:
Fragments of AF287270: 100-500, 6956-7356

Please also search the following sequences: SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7

441-460 = 1-20 SEQ ID 3

Thanks,
Steve

Stephen Kapushoc
Art Unit 1634 - USPTO
Tel: 571-272-3312
Office: REM 3A60
Mailbox: REM 2C70

09/851494

Goldin + Acierno

****
Searcher: Jan
Searcher Phone: 22504
Date Searcher Picked up: 1/12/06
Date completed: 1/17/06
Searcher Prep Time: 10
Online Time: 150

****
Type of Search
NA# C AA#:
S/L: C Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 14:53:29 ; Search time 1 Seconds
(without alignments)
2.849 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 GGGGTCTCAGCAGGGAACAA.....TAGCTCACTGCAGCCTCGAC 401

Scoring table: IDENTITY_NUC)
Gapop 10.0 , Gapext 0.5

Searched: 189 seqs, 3552 residues

Total number of hits satisfying chosen parameters: 378

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 189 summaries

Database : af287270_copy_100_500.rng4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	6.2	25	1	ADB84281	Human mucolipin (M
c	2	23	5.7	24	1	ABV75668	Human FB16-06 PCR
	3	22.4	5.6	24	1	ABL55369	Human leucine zipp
	4	21	5.2	21	1	ACA54779	Human NF-kappaB as
	5	21	5.2	21	1	ADU83270	Human NFkappaB-ass
c	6	20.4	5.1	22	1	AAT71928	Primer detects mar
c	7	20.4	5.1	22	1	AAT71925	Primer detects mar
c	8	20.4	5.1	22	1	AAT72000	Primer detects mar
c	9	20.4	5.1	22	1	AAT71997	Primer detects mar
	10	20.4	5.1	22	1	AAX83018	Primer K to isolat
	11	20.4	5.1	22	1	AAZ07500	AHRECASEPO transge
	12	20.4	5.1	22	1	AAD31456	Human chromosome 1
c	13	20	5.0	20	1	AAT73703	PCR primer SR1 use
c	14	20	5.0	20	1	AAA96410	Primer used to amp
c	15	20	5.0	20	1	AAA14945	PCR primer SR1 use
	16	20	5.0	20	1	ABZ99055	Human PDE4C oligon
	17	20	5.0	20	1	ABD32086	Human PDE4C-derive
	18	20	5.0	20	1	ADH77439	Human PTPN12 antis
	19	20	5.0	20	1	ADJ60940	Oligonucleotide as
	20	20	5.0	20	1	ADJ10322	Phosphorothioate a
	21	20	5.0	20	1	ADO46429	Human oligonucleot
	22	20	5.0	20	1	ADO13029	Single multiplex P
→	23	20	5.0	20	1	AEB28959	Human MCOLN1 gene
c	24	20	5.0	21	1	AAV27991	Ataxia-telangiecta
c	25	20	5.0	21	1	ADY84793	Human AGT-105 gene
c	26	19.4	4.8	21	1	AAX83014	Primer G to isolat
c	27	19.4	4.8	21	1	AAF17435	L1 cleavage site r
c	28	19.4	4.8	21	1	ADF12370	L1 retrotransposon
	29	19.4	4.8	21	1	ADH59619	Non-nucleotide pro
c	30	19	4.7	19	1	AAH37310	SNP specific lower
c	31	19	4.7	19	1	ADO14391	Human interleukin-
	32	19	4.7	19	1	ADO14519	Human interleukin-
c	33	19	4.7	19	1	ADW81468	MAP3K9 marker ampl
c	34	19	4.7	19	1	ADX86423	XIAP targeting siR
	35	19	4.7	19	1	ADX86890	XIAP targeting siR
c	36	19	4.7	20	1	AAZ37713	Human mdm2 phospho
c	37	19	4.7	20	1	AAZ21805	Exemplary oligonuc
c	38	19	4.7	20	1	AAF80867	Human mdm2 phospho
c	39	19	4.7	20	1	AAS29482	Human mdm2 antisen
c	40	19	4.7	20	1	ADD21678	Human mdm2 antisen
	41	19	4.7	20	1	ABZ98013	Human RANTES oligo
	42	19	4.7	20	1	ABD31044	Human RANTES-deriv
	43	19	4.7	20	1	ADJ59878	Oligonucleotide as
c	44	19	4.7	20	1	ADM14235	Human mPGES-1 chim
c	45	19	4.7	20	1	ADM14208	Human mPGES-1 chim
	46	19	4.7	20	1	ADO45368	Human oligonucleot
	47	19	4.7	20	1	ADZ42364	RT-PCR primer used
c	48	18.4	4.6	20	1	AAT65956	Primer #1 to ampli
c	49	18.4	4.6	20	1	AAZ37712	Human mdm2 phospho
c	50	18.4	4.6	20	1	AAZ37711	Human mdm2 phospho
c	51	18.4	4.6	20	1	AAF80866	Human mdm2 phospho
c	52	18.4	4.6	20	1	AAF80865	Human mdm2 phospho
c	53	18.4	4.6	20	1	AAH20695	Human telomeric re
c	54	18.4	4.6	20	1	AAS29480	Human mdm2 antisen
c	55	18.4	4.6	20	1	AAS29481	Human mdm2 antisen
c	56	18.4	4.6	20	1	AAD12408	Human caspase 8 mR
c	57	18.4	4.6	20	1	ABS67840	Human casein kinas
c	58	18.4	4.6	20	1	ADD21676	Human mdm2 antisen
c	59	18.4	4.6	20	1	ADD21677	Human mdm2 antisen
c	60	18.4	4.6	20	1	ADD25037	Human caspase-8 an
	61	18.4	4.6	20	1	ABZ98012	Human RANTES oligo
	62	18.4	4.6	20	1	ABZ99087	Human PDE4C oligon
	63	18.4	4.6	20	1	ABZ99103	Human PDE4C oligon
	64	18.4	4.6	20	1	ABD31043	Human RANTES-deriv
	65	18.4	4.6	20	1	ABD32134	Human PDE4C-derive
	66	18.4	4.6	20	1	ABD32118	Human PDE4C-derive
	67	18.4	4.6	20	1	ADJ59877	Oligonucleotide as
	68	18.4	4.6	20	1	ADJ60972	Oligonucleotide as
	69	18.4	4.6	20	1	ADJ60988	Oligonucleotide as
	70	18.4	4.6	20	1	ADJ96297	Human breast cance
c	71	18.4	4.6	20	1	ADJ96333	Human breast cance
	72	18.4	4.6	20	1	ADJ96393	Human breast cance
c	73	18.4	4.6	20	1	ADJ96457	Human breast cance
c	74	18.4	4.6	20	1	ADM14854	Human mPGES-1 chim
c	75	18.4	4.6	20	1	ADM14914	Human mPGES-1 chim
c	76	18.4	4.6	20	1	ADM14565	Human mPGES-1 chim
c	77	18.4	4.6	20	1	ADM15136	Human mPGES-1 chim
c	78	18.4	4.6	20	1	ADM15380	Human mPGES-1 chim
c	79	18.4	4.6	20	1	ADM14196	Human mPGES-1 chim
c	80	18.4	4.6	20	1	ADM14761	Human mPGES-1 chim
c	81	18.4	4.6	20	1	ADM15044	Human mPGES-1 chim
c	82	18.4	4.6	20	1	ADM14980	Human mPGES-1 chim
c	83	18.4	4.6	20	1	ADM15362	Human mPGES-1 chim
	84	18.4	4.6	20	1	ADO46461	Human oligonucleot
	85	18.4	4.6	20	1	ADO46477	Human oligonucleot
	86	18.4	4.6	20	1	ADO45367	Human oligonucleot
	87	18.4	4.6	20	1	ADW98085	Human breast cance
c	88	18.4	4.6	20	1	ADW98258	Human breast cance
c	89	18.4	4.6	20	1	ADW98121	Human breast cance
	90	18.4	4.6	20	1	ADW98194	Human breast cance
c	91	18.4	4.6	20	1	ADX82227	Melanoma associate
c	92	18.4	4.6	20	1	ADX82226	Melanoma associate
	93	18.4	4.6	20	1	ADY92906	PCR primer U479 us
c	94	18.2	4.5	19	1	AAQ25869	3' Alu primer. Sy
c	95	18.2	4.5	19	1	AAQ48683	Human Alu segment
c	96	18.2	4.5	19	1	AAQ85677	PCR primer alu 2 f
c	97	18.2	4.5	19	1	ADZ74318	Inter-Alu PCR prim
	98	18	4.5	18	1	ADY01152	Extend primer 28 u
	99	18	4.5	19	1	AAS01233	Forward PCR primer
	100	18	4.5	19	1	ADH89039	Human POLYX PCR pr
	101	18	4.5	19	1	ADY03156	Extend primer 606
	102	18	4.5	20	1	AAL61524	Human inhibitor-ka
c	103	17.8	4.4	19	1	ABX93650	Human Alu-specific
c	104	17.8	4.4	19	1	ABX95026	Human Alu specific
c	105	17.4	4.3	19	1	AAH39033	SNP specific upper
	106	17.4	4.3	19	1	AAH24568	Human Alu sequence

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c 107	17.4	4.3	19	1	ADY01278	Extend primer 154
c 108	17.4	4.3	19	1	ADX86792	XIAP targeting siR
109	17.4	4.3	19	1	ADX86325	XIAP targeting siR
110	17.4	4.3	19	1	AEB05389	Human IL-13RA1 siR
c 111	17.4	4.3	19	1	AEB05166	Human IL-13RA1 tra
112	17.4	4.3	19	1	AEC15226	Human IL-13RA1 siR
c 113	17.4	4.3	19	1	AEC15003	Human IL-13RA1 tra
c 114	17.2	4.3	19	1	AAQ76248	Generic primer fro
c 115	17	4.2	17	1	AAV29284	Nucleotide sequenc
c 116	17	4.2	17	1	AAC87597	Human Alu sequence
117	17	4.2	17	1	ADB44570	Tumour suppression
c 118	17	4.2	17	1	ACC51496	Human tumour suppr
119	17	4.2	17	1	ADL50193	Human PKR substrat
120	17	4.2	17	1	ADL50731	Human PKR substrat
121	17	4.2	17	1	ADL49907	Human PKR substrat
122	17	4.2	17	1	ADL49908	Human PKR substrat
123	17	4.2	17	1	ADL49909	Human PKR substrat
124	17	4.2	17	1	ADL49906	Human PKR substrat
125	17	4.2	17	1	ADL50192	Human PKR substrat
c 126	17	4.2	17	1	ADL82338	Human ER+ breast c
c 127	17	4.2	17	1	ADP08690	Extend primer 27 u
c 128	17	4.2	17	1	ADY01178	Extend primer 54 u
c 129	17	4.2	17	1	ADY00434	Extend primer 2 us
130	17	4.2	17	1	ADX82001	Melanoma associate
131	17	4.2	17	1	ADX81510	Melanoma associate
132	17	4.2	18	1	ADO56979	Human CARK/FPGT pr
133	17	4.2	18	1	ADO56561	Human cyclin-depen
c 134	16.4	4.1	18	1	AAZ27769	PCR primer for hum
c 135	16.4	4.1	18	1	ADY02910	Extend primer 360
136	16.4	4.1	18	1	ADY00671	Extend primer 239
137	16.4	4.1	18	1	ADY01277	Extend primer 153
c 138	16	4.0	16	1	AAF88161	Human thyroid malf
c 139	16	4.0	16	1	ACA62885	Repeated nucleic a
140	16	4.0	16	1	ACA62882	Repeated nucleic a
141	16	4.0	17	1	ADB04313	Human MDZ7 scannin
142	16	4.0	17	1	ADB04314	Human MDZ7 scannin
c 143	16	4.0	17	1	ACC63031	Murine oligonucleo
c 144	16	4.0	17	1	ADB44260	Tumour suppression
c 145	16	4.0	17	1	ACC51495	Human tumour suppr
146	16	4.0	17	1	ADL50732	Human PKR substrat
147	16	4.0	17	1	ADL49420	Human PKR substrat
148	16	4.0	17	1	ADX81033	Melanoma associate
149	15.4	3.8	17	1	AAA22718	Integrin subunit b
150	15.4	3.8	17	1	AAA22717	Integrin subunit b
c 151	15.4	3.8	17	1	ABT39409	Tumour suppression
152	15.4	3.8	17	1	ABT36213	Tumour suppression
c 153	15.4	3.8	17	1	ABT38720	Tumour suppression
c 154	15.4	3.8	17	1	ABT38728	Tumour suppression
155	15.4	3.8	17	1	ABT35457	Tumour suppression
c 156	15.4	3.8	17	1	ABT40068	Tumour suppression
c 157	15.4	3.8	17	1	ABT40150	Tumour suppression
c 158	15.4	3.8	17	1	ABT35874	Tumour suppression
159	15.4	3.8	17	1	ABZ60567	Human K-Ras DNAzym
c 160	15.4	3.8	17	1	ADB41143	Tumour suppression
161	15.4	3.8	17	1	ADB43523	Tumour suppression
c 162	15.4	3.8	17	1	ADB44518	Tumour suppression
c 163	15.4	3.8	17	1	ADE43565	Human IDE sequenci
c 164	15.4	3.8	17	1	ADI50915	Human tumour suppr
c 165	15.4	3.8	17	1	ADI50723	Human tumour suppr
c 166	15.4	3.8	17	1	ADI52180	Human tumour suppr
c 167	15.4	3.8	17	1	ADI50051	Human tumour suppr
c 168	15.4	3.8	17	1	ADI51643	Human tumour suppr
c 169	15.4	3.8	17	1	ACC52610	Human tumour suppr
c 170	15.4	3.8	17	1	ACC51497	Human tumour suppr
171	15.4	3.8	17	1	ACC52025	Human tumour suppr
c 172	15.4	3.8	17	1	ACC53324	Human tumour suppr
173	15.4	3.8	17	1	ADL49905	Human PKR substrat
174	15.4	3.8	17	1	ADL49419	Human PKR substrat
175	15.4	3.8	17	1	ADL49904	Human PKR substrat
176	15.4	3.8	17	1	ADL50191	Human PKR substrat
177	15.4	3.8	17	1	ADL50733	Human PKR substrat
c 178	15.4	3.8	17	1	ADH54043	Human neurodegener
c 179	15.4	3.8	17	1	ADK13186	Human glioma endot
c 180	15.4	3.8	17	1	ADL82349	Human ER+ breast c
181	15.4	3.8	17	1	ADZ29641	Human K-Ras substr
182	15.4	3.8	17	1	AEB71294	Extension primer f
183	15	3.7	15	1	AAF69438	Human IL4Ralpha ge
184	14	3.5	15	1	ABK98169	Triple helix formi
185	14	3.5	15	1	ABK98187	Triple helix formi
186	14	3.5	15	1	ABK98168	Triple helix formi
187	14	3.5	15	1	ABK98167	Triple helix formi
188	14	3.5	15	1	ABK98186	Triple helix formi
c 189	13.6	3.4	15	1	AAS98701	Colony stimulating

ALIGNMENTS

RESULT 1
ADB84281
ID ADB84281 standard; DNA; 25 BP.
XX
AC ADB84281;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human mucolipin (MCOLIPIN-1) gene AJ haplotype analysis primer #3.
XX
KW human; mucolipin; MCOLN-1; mucolipidosis IV; ion channel defect;
KW immunogen; gene therapy; ss; primer; PCR; AJ haplotype.
XX
OS Homo sapiens.
XX
PN US2003064363-A1.
XX
PD 03-APR-2003.
XX
PF 08-MAY-2001; 2001US-00851494.
XX
PR 18-AUG-2000; 2000US-0226388P.
XX
PA (MLFO-) ML4 FOUND & HAVARD COLLEGE.
XX
PI Goldin E, Slaugenhaupt SA, Sun M, Acierno JS;
XX
DR WPI; 2003-540779/51.
XX
PT New mucolipin (MCOLN1) polypeptides and nucleic acids, useful in gene
PT therapy for treating mucolipidosis IV or ion channel defect, or as
PT immunogen to generate antibodies that recognize the MCOLN1 polypeptide.
XX
PS Example; Page 18; 34pp; English.
XX
CC The invention describes a nucleic acid (I) encoding a mucolipin (MCOLN1)
CC polypeptide, and sharing at least 95% sequence identity with sequence
CC selected from 2 nucleotide sequences (designated S1 and S2, not given in
CC the specification). A mutation of in the MCOLN1 gene encoding the MCOLN1
CC polypeptide results in a defect in expression of a functional MCOLN1. The
CC MCOLN1 gene is useful for useful for the treatment of mucolipidosis IV or
CC ion channel defect. The MCOLN1 polypeptides are useful as immunogen to
CC generate antibodies that recognize the MCOLN1 polypeptide. Such
CC antibodies may be used for diagnostics and intracellular regulation of
CC MCOLN1 activity. The polynucleotides may also be useful in gene therapy.
CC This sequence represents a primer used to analyse the AJ haplotype of the
CC human mucolipin (MCOLN-1) gene.
XX
SQ Sequence 25 BP; 7 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 6.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        226 CTGATATAAATGGCAGGCAGCTTTC 250
              |||||||||||||||||||||||||
Db          1 CTGATATAAATGGCAGGCAGCTTTC 25
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 14:56:42 ; Search time 2 Seconds
(without alignments)
2.069 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 GGGGTCTCAGCAGGGAACAA.....TAGCTCACTGCAGCCTCGAC 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 244 seqs, 5160 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 244 summaries

Database : af287270_copy_100_500.rnpbm4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25.4	6.3	27	1	US-10-708-204-5106	Sequence 5106, Ap
c	2	25	6.2	25	1	US-10-956-157-173066	Sequence 173066,
	3	25	6.2	25	1	US-11-060-756-178198	Sequence 178198,
	4	24	6.0	24	1	US-10-708-204-5162	Sequence 5162, Ap
	5	24	6.0	25	1	US-10-956-157-185762	Sequence 185762,
	6	24	6.0	25	1	US-10-956-157-208929	Sequence 208929,
	7	24	6.0	25	1	US-11-060-756-178197	Sequence 178197,
	8	24	6.0	25	1	US-11-060-756-203216	Sequence 203216,
c	9	23.4	5.8	25	1	US-10-956-157-149516	Sequence 149516,
c	10	23.4	5.8	25	1	US-10-956-157-149517	Sequence 149517,
c	11	23.4	5.8	25	1	US-10-956-157-173133	Sequence 173133,
c	12	23.4	5.8	25	1	US-10-956-157-177068	Sequence 177068,
c	13	23.4	5.8	25	1	US-10-956-157-177069	Sequence 177069,
c	14	23.4	5.8	25	1	US-10-956-157-184259	Sequence 184259,
c	15	23.4	5.8	25	1	US-10-956-157-188388	Sequence 188388,
c	16	23.4	5.8	25	1	US-10-956-157-273920	Sequence 273920,
c	17	23.4	5.8	25	1	US-10-956-157-285780	Sequence 285780,
c	18	23.4	5.8	25	1	US-10-956-157-286030	Sequence 286030,
	19	23.4	5.8	25	1	US-10-956-157-287740	Sequence 287740,
	20	23.4	5.8	25	1	US-10-956-157-293223	Sequence 293223,
	21	23.4	5.8	25	1	US-10-956-157-293224	Sequence 293224,
	22	23.4	5.8	25	1	US-10-956-157-293225	Sequence 293225,
c	23	23.4	5.8	25	1	US-10-956-157-298488	Sequence 298488,
	24	23.4	5.8	25	1	US-10-708-204-5164	Sequence 5164, Ap
c	25	23.4	5.8	25	1	US-11-060-756-163912	Sequence 163912,
c	26	23.4	5.8	25	1	US-11-060-756-164006	Sequence 164006,
c	27	23.4	5.8	25	1	US-11-060-756-180494	Sequence 180494,
	28	23.4	5.8	25	1	US-11-060-756-200858	Sequence 200858,
c	29	23.4	5.8	25	1	US-11-060-756-272590	Sequence 272590,
	30	23.4	5.8	25	1	US-11-060-756-274785	Sequence 274785,
	31	23.4	5.8	25	1	US-11-060-756-278943	Sequence 278943,
	32	23.4	5.8	25	1	US-11-060-756-279896	Sequence 279896,
	33	23.4	5.8	25	1	US-11-060-756-279897	Sequence 279897,
c	34	23.4	5.8	25	1	US-11-060-756-287805	Sequence 287805,
	35	23	5.7	23	1	US-09-851-494B-10	Sequence 10, Appl
	36	23	5.7	23	1	US-10-708-204-5076	Sequence 5076, Ap
	37	23	5.7	23	1	US-10-708-204-5099	Sequence 5099, Ap
c	38	22	5.5	22	1	US-10-708-204-7	Sequence 7, Appli
c	39	22	5.5	22	1	US-10-708-204-13	Sequence 13, Appl
	40	22	5.5	22	1	US-10-708-204-72	Sequence 72, Appl
	41	22	5.5	22	1	US-10-708-204-91	Sequence 91, Appl
	42	22	5.5	22	1	US-10-708-204-195	Sequence 195, App
	43	22	5.5	22	1	US-10-708-204-208	Sequence 208, App
	44	22	5.5	22	1	US-10-708-204-771	Sequence 771, App
	45	22	5.5	22	1	US-10-708-204-1122	Sequence 1122, Ap
	46	22	5.5	22	1	US-10-708-204-1127	Sequence 1127, Ap
	47	22	5.5	22	1	US-10-708-204-1177	Sequence 1177, Ap
	48	22	5.5	22	1	US-10-708-204-1399	Sequence 1399, Ap
	49	22	5.5	22	1	US-10-708-204-1401	Sequence 1401, Ap
	50	22	5.5	22	1	US-10-708-204-1480	Sequence 1480, Ap
	51	22	5.5	22	1	US-10-708-204-1498	Sequence 1498, Ap
	52	22	5.5	22	1	US-10-708-204-2082	Sequence 2082, Ap
	53	22	5.5	22	1	US-10-708-204-2092	Sequence 2092, Ap
	54	22	5.5	22	1	US-10-708-204-2517	Sequence 2517, Ap
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	57	22	5.5	22	1	US-10-708-204-5075	Sequence 5075, Ap
	58	22	5.5	22	1	US-10-708-204-5086	Sequence 5086, Ap
	59	22	5.5	22	1	US-10-708-204-5095	Sequence 5095, Ap
	60	22	5.5	22	1	US-10-708-204-5098	Sequence 5098, Ap
	61	22	5.5	22	1	US-10-708-204-5105	Sequence 5105, Ap
	62	21.4	5.3	23	1	US-10-708-204-3821	Sequence 3821, Ap
	63	21.4	5.3	23	1	US-10-708-204-3863	Sequence 3863, Ap
	64	21.4	5.3	23	1	US-10-708-204-5124	Sequence 5124, Ap
	65	21	5.2	21	1	US-10-126-103-235	Sequence 235, App
	66	21	5.2	21	1	US-10-431-096-235	Sequence 235, App
	67	21	5.2	22	1	US-10-708-204-3851	Sequence 3851, Ap
	68	21	5.2	22	1	US-10-708-204-3870	Sequence 3870, Ap
	69	21	5.2	22	1	US-10-708-204-5096	Sequence 5096, Ap
	70	21	5.2	22	1	US-10-708-204-5165	Sequence 5165, Ap
	71	21	5.2	23	1	US-10-708-204-5097	Sequence 5097, Ap
	72	20.4	5.1	22	1	US-09-918-686-93	Sequence 93, Appl
	73	20.4	5.1	22	1	US-10-353-150-93	Sequence 93, Appl
	74	20.4	5.1	22	1	US-10-374-077-11	Sequence 11, Appl
c	75	20.4	5.1	22	1	US-10-708-204-14	Sequence 14, Appl
	76	20.4	5.1	22	1	US-10-708-204-73	Sequence 73, Appl
	77	20.4	5.1	22	1	US-10-708-204-75	Sequence 75, Appl
	78	20.4	5.1	22	1	US-10-708-204-162	Sequence 162, App
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c	83	20.4	5.1	22	1	US-10-708-204-460	Sequence 460, App
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c	86	20.4	5.1	22	1	US-10-708-204-480	Sequence 480, App
c	87	20.4	5.1	22	1	US-10-708-204-666	Sequence 666, App
	88	20.4	5.1	22	1	US-10-708-204-772	Sequence 772, App
c	89	20.4	5.1	22	1	US-10-708-204-872	Sequence 872, App
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c	95	20.4	5.1	22	1	US-10-708-204-1108	Sequence 1108, Ap
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	98	20.4	5.1	22	1	US-10-708-204-1400	Sequence 1400, Ap
	99	20.4	5.1	22	1	US-10-708-204-1478	Sequence 1478, Ap
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c	106	20.4	5.1	22	1	US-10-708-204-1587	Sequence 1587, Ap

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108	20.4	5.1	22	1	US-10-708-204-1720	Sequence 1720, Ap
109	20.4	5.1	22	1	US-10-708-204-1886	Sequence 1886, Ap
110	20.4	5.1	22	1	US-10-708-204-2091	Sequence 2091, Ap
c 111	20.4	5.1	22	1	US-10-708-204-2197	Sequence 2197, Ap
c 112	20.4	5.1	22	1	US-10-708-204-2207	Sequence 2207, Ap
c 113	20.4	5.1	22	1	US-10-708-204-2248	Sequence 2248, Ap
c 114	20.4	5.1	22	1	US-10-708-204-2249	Sequence 2249, Ap
c 115	20.4	5.1	22	1	US-10-708-204-2250	Sequence 2250, Ap
c 116	20.4	5.1	22	1	US-10-708-204-2252	Sequence 2252, Ap
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118	20.4	5.1	22	1	US-10-708-204-2518	Sequence 2518, Ap
119	20.4	5.1	22	1	US-10-708-204-3820	Sequence 3820, Ap
120	20.4	5.1	22	1	US-10-708-204-3827	Sequence 3827, Ap
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122	20.4	5.1	22	1	US-10-708-204-5114	Sequence 5114, Ap
c 123	20	5.0	20	1	US-10-085-906-302	Sequence 302, App
c 124	20	5.0	20	1	US-10-251-699-1	Sequence 1, Appli
125	20	5.0	20	1	US-10-172-911-80	Sequence 80, Appl
126	20	5.0	20	1	US-10-189-268-71	Sequence 71, Appl
127	20	5.0	20	1	US-10-754-446-3	Sequence 3, Appli
128	20	5.0	20	1	US-10-708-204-3841	Sequence 3841, Ap
129	20	5.0	20	1	US-10-708-204-5094	Sequence 5094, Ap
130	20	5.0	21	1	US-10-708-204-3869	Sequence 3869, Ap
131	20	5.0	21	1	US-10-708-204-5108	Sequence 5108, Ap
132	20	5.0	22	1	US-10-708-204-95	Sequence 95, Appl
133	20	5.0	22	1	US-10-708-204-202	Sequence 202, App
c 134	20	5.0	22	1	US-10-708-204-382	Sequence 382, App
c 135	20	5.0	22	1	US-10-708-204-483	Sequence 483, App
c 136	20	5.0	22	1	US-10-708-204-831	Sequence 831, App
c 137	20	5.0	22	1	US-10-708-204-876	Sequence 876, App
c 138	20	5.0	22	1	US-10-708-204-886	Sequence 886, App
c 139	20	5.0	22	1	US-10-708-204-1047	Sequence 1047, Ap
c 140	20	5.0	22	1	US-10-708-204-1102	Sequence 1102, Ap
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142	20	5.0	22	1	US-10-708-204-1176	Sequence 1176, Ap
143	20	5.0	22	1	US-10-708-204-1487	Sequence 1487, Ap
c 144	20	5.0	22	1	US-10-708-204-1539	Sequence 1539, Ap
c 145	20	5.0	22	1	US-10-708-204-1653	Sequence 1653, Ap
c 146	20	5.0	22	1	US-10-708-204-2243	Sequence 2243, Ap
c 147	20	5.0	22	1	US-10-708-204-2274	Sequence 2274, Ap
148	20	5.0	22	1	US-10-708-204-2548	Sequence 2548, Ap
c 149	20	5.0	22	1	US-10-708-204-4312	Sequence 4312, Ap
150	20	5.0	22	1	US-10-708-204-4381	Sequence 4381, Ap
151	20	5.0	22	1	US-10-708-204-4385	Sequence 4385, Ap
152	20	5.0	22	1	US-10-708-204-5072	Sequence 5072, Ap
c 153	19.4	4.8	21	1	US-10-085-906-401	Sequence 401, App
c 154	19.4	4.8	21	1	US-10-216-122-116	Sequence 116, App
155	19.4	4.8	21	1	US-10-255-434-25	Sequence 25, Appl
c 156	19.4	4.8	21	1	US-10-374-077-7	Sequence 7, Appli
157	19.4	4.8	21	1	US-10-708-204-3826	Sequence 3826, Ap
158	19	4.7	19	1	US-10-708-204-3840	Sequence 3840, Ap
159	19	4.7	19	1	US-10-708-204-3842	Sequence 3842, Ap
160	19	4.7	19	1	US-10-708-204-3854	Sequence 3854, Ap
161	19	4.7	19	1	US-10-708-204-4379	Sequence 4379, Ap
162	19	4.7	19	1	US-10-708-204-5110	Sequence 5110, Ap
163	19	4.7	19	1	US-10-708-204-5172	Sequence 5172, Ap
c 164	19	4.7	20	1	US-09-752-983-243	Sequence 243, App
c 165	19	4.7	20	1	US-09-863-806-155	Sequence 155, App
c 166	19	4.7	20	1	US-10-005-344-243	Sequence 243, App
c 167	19	4.7	20	1	US-10-671-395-395	Sequence 395, App
c 168	19	4.7	20	1	US-10-671-395-422	Sequence 422, App
c 169	19	4.7	20	1	US-10-754-478-155	Sequence 155, App
170	19	4.7	20	1	US-10-708-204-3868	Sequence 3868, Ap
171	19	4.7	21	1	US-10-708-204-4384	Sequence 4384, Ap
172	19	4.7	21	1	US-10-708-204-5102	Sequence 5102, Ap
c 173	18.4	4.6	20	1	US-09-752-983-241	Sequence 241, App
c 174	18.4	4.6	20	1	US-09-752-983-242	Sequence 242, App
c 175	18.4	4.6	20	1	US-10-181-177-94	Sequence 94, Appl
c 176	18.4	4.6	20	1	US-10-005-344-241	Sequence 241, App
c 177	18.4	4.6	20	1	US-10-005-344-242	Sequence 242, App
c 178	18.4	4.6	20	1	US-10-148-355A-64	Sequence 64, Appl
179	18.4	4.6	20	1	US-10-199-676-38	Sequence 38, Appl
c 180	18.4	4.6	20	1	US-10-199-676-74	Sequence 74, Appl
c 181	18.4	4.6	20	1	US-10-671-395-383	Sequence 383, App
c 182	18.4	4.6	20	1	US-10-671-395-752	Sequence 752, App
c 183	18.4	4.6	20	1	US-10-671-395-948	Sequence 948, App
c 184	18.4	4.6	20	1	US-10-671-395-1041	Sequence 1041, Ap
c 185	18.4	4.6	20	1	US-10-671-395-1101	Sequence 1101, Ap
c 186	18.4	4.6	20	1	US-10-671-395-1167	Sequence 1167, Ap
c 187	18.4	4.6	20	1	US-10-671-395-1231	Sequence 1231, Ap
c 188	18.4	4.6	20	1	US-10-671-395-1323	Sequence 1323, Ap
c 189	18.4	4.6	20	1	US-10-671-395-1549	Sequence 1549, Ap
c 190	18.4	4.6	20	1	US-10-671-395-1567	Sequence 1567, Ap
191	18.4	4.6	20	1	US-10-639-300-38	Sequence 38, Appl
c 192	18.4	4.6	20	1	US-10-639-300-74	Sequence 74, Appl
c 193	18.4	4.6	20	1	US-10-840-590-1509	Sequence 1509, Ap
c 194	18.4	4.6	20	1	US-10-840-590-1510	Sequence 1510, Ap
c 195	18.2	4.5	19	1	US-10-831-819-7	Sequence 7, Appli
196	18	4.5	18	1	US-10-708-204-5101	Sequence 5101, Ap
197	18	4.5	19	1	US-10-098-871-37	Sequence 37, Appl
198	18	4.5	19	1	US-10-800-487-155	Sequence 155, App
c 199	18	4.5	19	1	US-10-800-487-321	Sequence 321, App
200	18	4.5	19	1	US-10-923-181-155	Sequence 155, App
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202	18	4.5	20	1	US-09-993-731-22	Sequence 22, Appl
203	18	4.5	20	1	US-10-708-204-4383	Sequence 4383, Ap
204	18	4.5	20	1	US-10-708-204-5092	Sequence 5092, Ap
c 205	17.4	4.3	19	1	US-10-863-973-922	Sequence 922, App
206	17.4	4.3	19	1	US-10-863-973-1145	Sequence 1145, Ap
c 207	17.4	4.3	19	1	US-10-922-675-922	Sequence 922, App
208	17.4	4.3	19	1	US-10-922-675-1145	Sequence 1145, Ap
c 209	17.4	4.3	19	1	US-11-014-373-190	Sequence 190, App
210	17.4	4.3	19	1	US-11-014-373-467	Sequence 467, App
c 211	17.2	4.3	18	1	US-10-463-981B-2	Sequence 2, Appli
c 212	17	4.2	17	1	US-09-242-772-1	Sequence 1, Appli
213	17	4.2	17	1	US-10-156-306-1651	Sequence 1651, Ap
214	17	4.2	17	1	US-10-156-306-1652	Sequence 1652, Ap
215	17	4.2	17	1	US-10-156-306-1653	Sequence 1653, Ap
216	17	4.2	17	1	US-10-156-306-1654	Sequence 1654, Ap
217	17	4.2	17	1	US-10-156-306-2389	Sequence 2389, Ap
218	17	4.2	17	1	US-10-156-306-2390	Sequence 2390, Ap
219	17	4.2	17	1	US-10-156-306-3776	Sequence 3776, Ap
c 220	17	4.2	17	1	US-10-339-782-309	Sequence 309, App
221	17	4.2	17	1	US-10-704-513-302	Sequence 302, App
222	17	4.2	17	1	US-10-704-513-720	Sequence 720, App
223	17	4.2	17	1	US-10-840-590-793	Sequence 793, App
224	17	4.2	17	1	US-10-840-590-1284	Sequence 1284, Ap
c 225	16.4	4.1	18	1	US-09-784-423-69	Sequence 69, Appl
226	16.4	4.1	18	1	US-10-708-204-3825	Sequence 3825, Ap
227	16	4.0	16	1	US-09-739-909-8	Sequence 8, Appli
c 228	16	4.0	16	1	US-09-739-909-11	Sequence 11, Appl
229	16	4.0	17	1	US-10-156-306-534	Sequence 534, App
230	16	4.0	17	1	US-10-156-306-3777	Sequence 3777, Ap
231	16	4.0	17	1	US-10-703-817-224	Sequence 224, App
232	16	4.0	17	1	US-10-840-590-314	Sequence 314, App
233	15.4	3.8	17	1	US-10-156-306-533	Sequence 533, App
234	15.4	3.8	17	1	US-10-156-306-1649	Sequence 1649, Ap
235	15.4	3.8	17	1	US-10-156-306-1650	Sequence 1650, Ap
236	15.4	3.8	17	1	US-10-156-306-2388	Sequence 2388, Ap
237	15.4	3.8	17	1	US-10-156-306-3778	Sequence 3778, Ap
238	15.4	3.8	17	1	US-10-238-700-679	Sequence 679, App
c 239	15.4	3.8	17	1	US-10-339-782-320	Sequence 320, App
c 240	15.4	3.8	17	1	US-10-339-793-16	Sequence 16, Appl
c 241	15.4	3.8	17	1	US-10-282-174-170	Sequence 170, App
c 242	15.4	3.8	17	1	US-10-600-009-170	Sequence 170, App
243	15.4	3.8	17	1	US-10-724-270-679	Sequence 679, App
244	15	3.7	15	1	US-10-010-802-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-10-708-204-5106
; Sequence 5106, Application US/10708204

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 14:58:13 ; Search time 0.001 Seconds
(without alignments)
318.394 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 GGGGTCTCAGCAGGGAACAA.....TAGCTCACTGCAGCCTCGAC 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 397 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 19 summaries

Database : af287270_copy_100_500.rnpbn4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	23.4	5.8	25	1	US-11-121-849-17198	Sequence 17198, A
c	2	23.4	5.8	25	1	US-11-121-849-44508	Sequence 44508, A
c	3	23.4	5.8	25	1	US-11-121-849-44509	Sequence 44509, A
c	4	23.4	5.8	25	1	US-11-121-849-48982	Sequence 48982, A
c	5	23.4	5.8	25	1	US-11-121-849-48983	Sequence 48983, A
c	6	23.4	5.8	25	1	US-11-121-849-48984	Sequence 48984, A
c	7	23.4	5.8	25	1	US-11-121-849-48985	Sequence 48985, A
	8	20	5.0	20	1	US-10-515-538-80	Sequence 80, Appl
	9	19	4.7	20	1	US-10-353-783-33	Sequence 33, Appl
	10	18	4.5	18	1	US-10-857-780-2580	Sequence 2580, Ap
	11	18	4.5	19	1	US-10-857-780-4587	Sequence 4587, Ap
c	12	17.4	4.3	19	1	US-10-857-780-2706	Sequence 2706, Ap
c	13	17.4	4.3	19	1	US-11-001-347-922	Sequence 922, App
	14	17.4	4.3	19	1	US-11-001-347-1145	Sequence 1145, Ap
c	15	17	4.2	17	1	US-10-857-780-1868	Sequence 1868, Ap
c	16	17	4.2	17	1	US-10-857-780-2606	Sequence 2606, Ap
	17	16.4	4.1	18	1	US-10-857-780-2105	Sequence 2105, Ap
	18	16.4	4.1	18	1	US-10-857-780-2705	Sequence 2705, Ap
c	19	16.4	4.1	18	1	US-10-857-780-4341	Sequence 4341, Ap

ALIGNMENTS

RESULT 1
US-11-121-849-17198/c
; Sequence 17198, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 17198
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-17198

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         25 TCTTGCTCTGTTGCCCAAGCTGGAG 1
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RESULT 2
US-11-121-849-44508/c
; Sequence 44508, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44508
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44508

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         25 TGGTGTGATGATAGCTCACTGCAGC 1
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RESULT 3
US-11-121-849-44509/c
; Sequence 44509, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44509
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44509

Query Match 5.8%; Score 23.4; DB 1; Length 25;

Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        465 TGCAGTGGTGTGATCATAGCTCACT 489
              ||||||||||||||| ||||||||||
Db         25 TGCAGTGGTGTGATGATAGCTCACT 1
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RESULT 4
US-11-121-849-48982/c
; Sequence 48982, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48982
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-48982

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        447 CTGTTGCCCAGGCTGGAGTGCAGTG 471
              |||| ||||||||||||||||||||||
Db         25 CTGTCGCCCAGGCTGGAGTGCAGTG 1
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RESULT 5
US-11-121-849-48983/c
; Sequence 48983, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48983
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-48983

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        446 TCTGTTGCCCAGGCTGGAGTGCAGT 470
              ||||| ||||||||||||||||||||
Db         25 TCTGTCGCCCAGGCTGGAGTGCAGT 1
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RESULT 6
US-11-121-849-48984/c
; Sequence 48984, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sa
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-48984

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        445 CTCTGTTGCCCAGGCTGGAGTGCAG 469
              |||||| ||||||||||||||||||||
Db         25 CTCTGTCGCCCAGGCTGGAGTGCAG 1
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RESULT 7
US-11-121-849-48985/c
; Sequence 48985, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sa
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48985
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-48985

Query Match 5.8%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        444 GCTCTGTTGCCCAGGCTGGAGTGCA 468
              ||||||| ||||||||||||||||||
Db         25 GCTCTGTCGCCCAGGCTGGAGTGCA 1
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RESULT 8
US-10-515-538-80
; Sequence 80, Application US/10515538
; Publication No. US20050282760A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Lex M. Cowsert
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN12 EXPRESSION
; FILE REFERENCE: PTS-0016USA
; CURRENT APPLICATION NUMBER: US/10/515,538
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 10/172,911
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/18707
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 80

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 14:54:56 ; Search time 0.001 Seconds
(without alignments)
874.180 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 GGGGTCTCAGCAGGGAACAA.....TAGCTCACTGCAGCCTCGAC 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 58 seqs, 1090 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 58 summaries

Database : af287270_copy_100_500.rni4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20.4	5.1	22	1	US-08-599-252-35	Sequence 35, Appl
c	2	20.4	5.1	22	1	US-08-599-252-38	Sequence 38, Appl
	3	20.4	5.1	22	1	US-08-291-074-2	Sequence 2, Appli
	4	20.4	5.1	22	1	US-08-781-891-11	Sequence 11, Appl
	5	20.4	5.1	22	1	US-09-918-686-93	Sequence 93, Appl
	6	20.4	5.1	22	1	US-09-618-166-11	Sequence 11, Appl
c	7	20.4	5.1	22	1	PCT-US96-06352-35	Sequence 35, Appl
c	8	20.4	5.1	22	1	PCT-US96-06352-38	Sequence 38, Appl
c	9	20.4	5.1	22	1	PCT-US96-06583-35	Sequence 35, Appl
c	10	20.4	5.1	22	1	PCT-US96-06583-38	Sequence 38, Appl
c	11	20	5.0	20	1	US-09-418-804-1	Sequence 1, Appli
	12	20	5.0	20	1	US-10-172-911-80	Sequence 80, Appl
c	13	20	5.0	20	1	US-10-251-699-1	Sequence 1, Appli
c	14	20	5.0	21	1	US-08-753-147-28	Sequence 28, Appl
c	15	19.4	4.8	21	1	US-08-781-891-7	Sequence 7, Appli
c	16	19.4	4.8	21	1	US-08-847-844A-116	Sequence 116, App
c	17	19.4	4.8	21	1	US-09-618-166-7	Sequence 7, Appli
c	18	19	4.7	20	1	US-09-280-805-243	Sequence 243, App
c	19	19	4.7	20	1	US-09-038-637-155	Sequence 155, App
	20	19	4.7	20	1	US-09-224-683-33	Sequence 33, Appl
	21	19	4.7	20	1	US-09-604-325A-33	Sequence 33, Appl
c	22	18.4	4.6	20	1	US-08-222-177A-274	Sequence 274, App
c	23	18.4	4.6	20	1	US-09-280-805-241	Sequence 241, App
c	24	18.4	4.6	20	1	US-09-280-805-242	Sequence 242, App
c	25	18.4	4.6	20	1	US-09-487-445-94	Sequence 94, Appl
c	26	18.4	4.6	20	1	US-09-467-642-64	Sequence 64, Appl
c	27	18.4	4.6	20	1	US-09-780-173A-18	Sequence 18, Appl
c	28	18.2	4.5	19	1	US-08-070-517-2	Sequence 2, Appli
c	29	18.2	4.5	19	1	US-08-118-441-2	Sequence 2, Appli
c	30	18.2	4.5	19	1	US-08-422-699A-14	Sequence 14, Appl
c	31	18.2	4.5	19	1	US-08-422-706B-14	Sequence 14, Appl
c	32	18.2	4.5	19	1	US-08-338-579A-2	Sequence 2, Appli
c	33	18.2	4.5	19	1	PCT-US94-09851-2	Sequence 2, Appli
	34	17.4	4.3	19	1	US-09-366-840-2	Sequence 2, Appli
	35	17.2	4.3	19	1	US-10-176-884-44	Sequence 44, Appl
c	36	17	4.2	17	1	US-08-635-820A-2	Sequence 2, Appli
c	37	17	4.2	17	1	US-09-100-104-2	Sequence 2, Appli
	38	17	4.2	17	1	US-10-054-295-132	Sequence 132, App
	39	17	4.2	17	1	US-09-438-486A-132	Sequence 132, App
	40	17	4.2	18	1	US-09-979-275A-7	Sequence 7, Appli
c	41	16.4	4.1	18	1	US-09-018-584A-69	Sequence 69, Appl
c	42	16.4	4.1	18	1	US-09-784-423-69	Sequence 69, Appl
	43	16.2	4.0	18	1	US-09-981-397A-1	Sequence 1, Appli
	44	16	4.0	16	1	US-10-203-780-9	Sequence 9, Appli
c	45	16	4.0	16	1	US-10-054-295-131	Sequence 131, App
c	46	16	4.0	16	1	US-09-438-486A-131	Sequence 131, App
	47	16	4.0	16	1	US-10-227-001-21	Sequence 21, Appl
	48	16	4.0	16	1	US-10-072-975-9	Sequence 9, Appli
	49	16	4.0	17	1	US-09-730-559B-107	Sequence 107, App
	50	15	3.7	15	1	US-09-850-982B-4	Sequence 4, Appli
	51	15	3.7	15	1	US-09-793-146-54	Sequence 54, Appl
	52	15	3.7	15	1	US-09-793-146-55	Sequence 55, Appl
	53	15	3.7	15	1	US-10-227-001-23	Sequence 23, Appl
	54	15	3.7	15	1	US-10-384-450A-5	Sequence 5, Appli
	55	15	3.7	15	1	US-10-072-975-10	Sequence 10, Appl
	56	15	3.7	16	1	US-10-227-001-20	Sequence 20, Appl
	57	14.4	3.6	16	1	US-09-479-005A-260	Sequence 260, App
	58	14	3.5	15	1	US-10-227-001-24	Sequence 24, Appl

ALIGNMENTS

```
RESULT 1
US-08-599-252-35/c
; Sequence 35, Application US/08599252
; Patent No. 5705343
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,252
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
US-08-599-252-35

  Query Match             5.1%;  Score 20.4;  DB 1;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        444 GCTCTGTTGCCCAGGCTGGAGT 465
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Db         22 GCTCTATTGCCCAGGCTGGAGT 1


RESULT 2
US-08-599-252-38/c
; Sequence 38, Application US/08599252
; Patent No. 5705343
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,252
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-599-252-38

  Query Match             5.1%;  Score 20.4;  DB 1;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        444 GCTCTGTTGCCCAGGCTGGAGT 465
              ||||| ||||||||||||||||
Db         22 GCTCTATTGCCCAGGCTGGAGT 1


RESULT 3
US-08-291-074-2
; Sequence 2, Application US/08291074
; Patent No. 5959171
;  GENERAL INFORMATION:
;    APPLICANT:  Hyttinen, Juha-Matti
;    APPLICANT:  Korhonen, Veli-Pekka
;    APPLICANT:  Janne, Juhani
;    TITLE OF INVENTION:  METHOD FOR THE PRODUCTION OF
;    TITLE OF INVENTION:  BIOLOGICALLY ACTIVE POLYPEPTIDES IN A MAMMAL'S MILK AS
;    TITLE OF INVENTION:  FUSION PROTEINS THAT ARE LESS ACTIVE THAN THE FREE
;    TITLE OF INVENTION:  POLYPEPTIDES, OR NON-ACTIVE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Adduci, Mastriani, Schaumberg & Schill
;      STREET:  1140 Connecticut Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  U.S.A.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/291,074
;      FILING DATE:  17-AUG-1994
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubovcik, Ronald J.
;      REGISTRATION NUMBER:  25,401
;      REFERENCE/DOCKET NUMBER:  TUR-017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-6300
;      TELEFAX:  202-466-2006
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-291-074-2

  Query Match             5.1%;  Score 20.4;  DB 1;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        464 GTGCAGTGGTGTGATCATAGCT 485
              |||||||||||||||||| ||||
Db          1 GTGCAGTGGTGTGATCACAGCT 22


RESULT 4
US-08-781-891-11
; Sequence 11, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 15:00:13 ; Search time 0.001 Seconds
(without alignments)
13.634 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 CAGTGGGCGGATCCCCATCA.....CATCCTTGGCCCTACCCGCT 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 17 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : af287270_copy_6956_7356.rge4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
c 1	15.4	3.8	17	1	AX757826	ACCESSION:AX757826

ALIGNMENTS

RESULT 1
AX757826/c
LOCUS AX757826 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1147 from Patent WO03040369.
ACCESSION AX757826
VERSION AX757826.1 GI:32252442
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 1147 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.8%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       7175 CGTCCTGTGCTGAGATC 7191
              ||||||| |||||||||
Db         17 CGTCCTGGGCTGAGATC 1
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Search completed: January 17, 2006, 15:00:13
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 15:01:31 ; Search time 0.001 Seconds
(without alignments)
112.280 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 CAGTGGGCGGATCCCCATCA.....CATCCTTGGCCCTACCCGCT 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 140 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database : af287270_copy_6956_7356.rng4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	5.2	21	1	ADU28709	Knock-down target
c 2	21	5.2	21	1	AEB28960	Human MCOLN1 gene
c 3	20	5.0	20	1	ADB84282	Human mucolipin (M
4	16	4.0	16	1	AEB28963	Human MCOLN1 gene
c 5	15.4	3.8	17	1	ADB40824	Tumour suppression
6	14	3.5	15	1	ACD66351	Anti-HCV nucleic a
7	14	3.5	15	1	ACD66421	Anti-HCV enzymatic
8	14	3.5	15	1	ADI87738	Anti-HCV molecule

ALIGNMENTS

RESULT 1
ADU28709
ID ADU28709 standard; DNA; 21 BP.
XX
AC ADU28709;
XX
DT 27-JAN-2005 (first entry)
XX
DE Knock-down target sequence #2107.
XX
KW ds; RNA production; protein production; drug development;
KW knock-down target.
XX
OS Unidentified.
XX
PN WO2004094636-A1.
XX
PD 04-NOV-2004.
XX
PF 24-APR-2003; 2003WO-EP004362.
XX
PR 24-APR-2003; 2003WO-EP004362.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
PA (VSCH/) VAN DER SCHUEREN J.
XX
PI Arts GJF, Lambrecht MJY, Djokic K, Clasen RJ, Mesic E;
PI Griffioen S, Bergs CJL;
XX
DR WPI; 2004-775940/76.
XX
PT New knockdown sequences, useful in lowering the amount of RNA and/or
PT protein production in cells used in drug development process.
XX
PS Claim 11; SEQ ID NO 2123; 402pp; English.
XX
CC The invention relates to a polynucleotide comprising an RNA sequence. The
CC polynucleotides, vector, libraries, and method are useful in lowering the
CC amount of RNA and/or protein production in cells used in drug development
CC process. The present sequence represents a knock-down target sequence.
XX
SQ Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 5.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6994 ACATCCAGGAGTGTAAGCACC 7014
||||||||||||||||||||
Db 1 ACATCCAGGAGTGTAAGCACC 21

RESULT 2
AEB28960/c
ID AEB28960 standard; DNA; 21 BP.
XX
AC AEB28960;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene PCR primer PRI R2 SEQ ID NO:4.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 1; SEQ ID NO 4; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in

```
CC   donor fluorophore fluorescence or decrease in acceptor fluorophore
CC   fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC   described: (1) an oligonucleotide (ON1) comprising a sequence
CC   complementary to the coding or non-coding strand of the mucolipin-1
CC   (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC   sequences, comprising ON1. (M1) is useful for determining the presence of
CC   ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC   is useful for genetic counseling of individuals at risk for ML IV or at
CC   risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC   on chromosome 19p13. The present sequence represents a PCR primer for the
CC   MCOLN1 gene, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 21 BP; 5 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             5.2%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.71;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7017 AGTGTCTTCCAGCACGGTGAG 7037
             |||||||||||||||||||||
Db         21 AGTGTCTTCCAGCACGGTGAG 1


RESULT 3
ADB84282/c
ID   ADB84282 standard; DNA; 20 BP.
XX
AC   ADB84282;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human mucolipin (MCOLIPIN-1) gene AJ haplotype analysis primer #4.
XX
KW   human; mucolipin; MCOLN-1; mucolipidosis IV; ion channel defect;
KW   immunogen; gene therapy; ss; primer; PCR; AJ haplotype.
XX
OS   Homo sapiens.
XX
PN   US2003064363-A1.
XX
PD   03-APR-2003.
XX
PF   08-MAY-2001; 2001US-00851494.
XX
PR   18-AUG-2000; 2000US-0226388P.
XX
PA   (MLFO-) ML4 FOUND & HAVARD COLLEGE.
XX
PI   Goldin E,  Slaugenhaupt SA,  Sun M,  Acierno JS;
XX
DR   WPI; 2003-540779/51.
XX
PT   New mucolipin (MCOLN1) polypeptides and nucleic acids, useful in gene
PT   therapy for treating mucolipidosis IV or ion channel defect, or as
PT   immunogen to generate antibodies that recognize the MCOLN1 polypeptide.
XX
PS   Example; Page 18; 34pp; English.
XX
CC   The invention describes a nucleic acid (I) encoding a mucolipin (MCOLN1)
CC   polypeptide, and sharing at least 95% sequence identity with sequence
CC   selected from 2 nucleotide sequences (designated S1 and S2, not given in
CC   the specification). A mutation of in the MCOLN1 gene encoding the MCOLN1
CC   polypeptide results in a defect in expression of a functional MCOLN1. The
CC   MCOLN1 gene is useful for useful for the treatment of mucolipidosis IV or
CC   ion channel defect. The MCOLN1 polypeptides are useful as immunogen to
CC   generate antibodies that recognize the MCOLN1 polypeptide. Such
CC   antibodies may be used for diagnostics and intracellular regulation of
CC   MCOLN1 activity. The polynucleotides may also be useful in gene therapy.
CC   This sequence represents a primer used to analyse the AJ haplotype of the
CC   human mucolipin (MCOLN-1) gene.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             5.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7018 GTGTCTTCCAGCACGGTGAG 7037
             ||||||||||||||||||||
Db         20 GTGTCTTCCAGCACGGTGAG 1


RESULT 4
AEB28963
ID   AEB28963 standard; DNA; 16 BP.
XX
AC   AEB28963;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human MCOLN1 gene probe DEL SEQ ID NO:7.
XX
KW   mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; probe;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US2005153300-A1.
XX
PD   14-JUL-2005.
XX
PF   09-JAN-2004; 2004US-00754446.
XX
PR   09-JAN-2004; 2004US-00754446.
XX
PA   (QUES-) QUEST DIAGNOSTICS INC.
XX
PI   Sun W,  Hantash F;
XX
DR   WPI; 2005-521160/53.
XX
PT   Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT   amplifying the nucleic acid, detecting amplified product with labeled
PT   oligonucleotide probes via a change in fluorescence which indicates the
PT   presence of an ML IV mutant.
XX
PS   Claim 3; SEQ ID NO 7; 15pp; English.
XX
CC   The invention relates to a method (M1) for detecting the presence of
CC   mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC   involves contacting the nucleic acid with oligonucleotide primers and
CC   probes, conducting amplification by temperature cycling and monitoring
CC   the accumulation of amplified nucleic acid by detecting an increase in
CC   donor fluorophore fluorescence or decrease in acceptor fluorophore
CC   fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC   described: (1) an oligonucleotide (ON1) comprising a sequence
CC   complementary to the coding or non-coding strand of the mucolipin-1
CC   (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC   sequences, comprising ON1. (M1) is useful for determining the presence of
CC   ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC   is useful for genetic counseling of individuals at risk for ML IV or at
CC   risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC   on chromosome 19p13. The present sequence represents a probe for the
CC   MCOLN1 gene, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 16 BP; 5 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             4.0%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6982 AGACCCAGGCCCACAT 6997
             ||||||||||||||||
Db          1 AGACCCAGGCCCACAT 16
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 15:03:21 ; Search time 0.001 Seconds
(without alignments)
147.568 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 CAGTGGGCGGATCCCCATCA.....CATCCTTGGCCCTACCCGCT 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 10 seqs, 184 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : af287270_copy_6956_7356.rnpbm4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	6.2	25	1	US-11-060-756-186093	Sequence 186093,
	2	25	6.2	25	1	US-11-060-756-261208	Sequence 261208,
c	3	21	5.2	21	1	US-10-754-446-4	Sequence 4, Appli
c	4	20	5.0	20	1	US-09-851-494B-11	Sequence 11, Appl
	5	16	4.0	16	1	US-10-754-446-7	Sequence 7, Appli
c	6	14.4	3.6	16	1	US-09-896-324B-62	Sequence 62, Appl
c	7	14.4	3.6	16	1	US-10-236-363A-44	Sequence 44, Appl
	8	14	3.5	15	1	US-09-740-332-4784	Sequence 4784, Ap
	9	14	3.5	15	1	US-09-817-879-4784	Sequence 4784, Ap
	10	14	3.5	15	1	US-10-669-841-7381	Sequence 7381, Ap

ALIGNMENTS

RESULT 1
US-11-060-756-186093
; Sequence 186093, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-186093

Query Match 6.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       6991 CCCACATCCAGGAGTGTAAGCACCC 7015
             |||||||||||||||||||||||||
Db          1 CCCACATCCAGGAGTGTAAGCACCC 25
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RESULT 2
US-11-060-756-261208
; Sequence 261208, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-261208

Query Match 6.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       6989 GGCCCACATCCAGGAGTGTAAGCAC 7013
             |||||||||||||||||||||||||
Db          1 GGCCCACATCCAGGAGTGTAAGCAC 25
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RESULT 3
US-10-754-446-4/c
; Sequence 4, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-754-446-4

Query Match 5.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       7017 AGTGTCTTCCAGCACGGTGAG 7037
             |||||||||||||||||||||
Db         21 AGTGTCTTCCAGCACGGTGAG 1
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RESULT 4
US-09-851-494B-11/c

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; Sequence 11, Application US/09851494B
; Publication No. US20030064363A1
; GENERAL INFORMATION:
;  APPLICANT: ML4 Foundation
;  APPLICANT:  Goldin, Ehud
;  APPLICANT:  Slaugenhaupt, Susan A.
;  APPLICANT:  Sun, Mei
;  APPLICANT:  Acierno, James S.
;  TITLE OF INVENTION: A Gene Encoding A New TRP Channel is Mutated in Mucolipidosis IV
;  FILE REFERENCE: 3394/1H557US1
;  CURRENT APPLICATION NUMBER: US/09/851,494B
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-851-494B-11

  Query Match             5.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7018 GTGTCTTCCAGCACGGTGAG 7037
             ||||||||||||||||||||
Db         20 GTGTCTTCCAGCACGGTGAG 1


RESULT 5
US-10-754-446-7
; Sequence 7, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
;  APPLICANT: SUN, WEIMIN
;  APPLICANT:  HANTASH, FERAS
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
;  TITLE OF INVENTION:  MUCOLIPIDOSIS IV MUTATIONS
;  FILE REFERENCE: 034827-2301
;  CURRENT APPLICATION NUMBER: US/10/754,446
;  CURRENT FILING DATE:  2004-01-09
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-754-446-7

  Query Match             4.0%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6982 AGACCCAGGCCCACAT 6997
             ||||||||||||||||
Db          1 AGACCCAGGCCCACAT 16


RESULT 6
US-09-896-324B-62/c
; Sequence 62, Application US/09896324B
; Publication No. US20030148276A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Bi-yu
;  TITLE OF INVENTION: METHOD FOR IDENTIFICATION, SEPARATION AND QUANTITATIVE MEASUREMEN
;  TITLE OF INVENTION:  NUCLEIC ACID FRAGMENTS
;  FILE REFERENCE: 45163-1008
;  CURRENT APPLICATION NUMBER: US/09/896,324B
;  CURRENT FILING DATE:  2002-11-04
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: CD18-BsaJ I-ga
US-09-896-324B-62

  Query Match             3.6%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 5.9;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7176 GTCCTGTGCTGAGATC 7191
             |||| ||||||||||||
Db         16 GTCCAGTGCTGAGATC 1


RESULT 7
US-10-236-363A-44/c
; Sequence 44, Application US/10236363A
; Publication No. US20030165923A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Bi-yu
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Shi, Liang
;  TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF GENETIC MARKERS
;  FILE REFERENCE: TM0011-CIP
;  CURRENT APPLICATION NUMBER: US/10/236,363A
;  CURRENT FILING DATE:  2002-11-19
;  PRIOR APPLICATION NUMBER: US 09/896,324
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,596
;  PRIOR FILING DATE: 2000-06-30
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: adapter oligonucleotide
US-10-236-363A-44

  Query Match             3.6%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 5.9;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       7176 GTCCTGTGCTGAGATC 7191
             |||| ||||||||||||
Db         16 GTCCAGTGCTGAGATC 1


RESULT 8
US-09-740-332-4784
; Sequence 4784, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: RPI 400/003
;  CURRENT APPLICATION NUMBER: US/09/740,332
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9704
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4784
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 15:04:33 ; Search time 0.001 Seconds
(without alignments)
63.358 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 CAGTGGGCGGATCCCCATCA.....CATCCTTGGCCCTACCCGCT 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 79 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : af287270_copy_6956_7356.rnpbn4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	5.0	21	1	US-10-310-914A-66074	Sequence 66074, A
	2	18.4	4.6	20	1	US-10-310-914A-253105	Sequence 253105,
c	3	18	4.5	20	1	US-10-310-914A-66019	Sequence 66019, A
	4	17	4.2	18	1	US-10-310-914A-918753	Sequence 918753,

ALIGNMENTS

RESULT 1
US-10-310-914A-66074/c
; Sequence 66074, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66074
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-66074

Query Match 5.0%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       7057 CACTGACCAGGGGCCCTGGC 7076
             ||||||||||||||||||||
Db         20 CACTGACCAGGGGCCCTGGC 1
```

RESULT 2
US-10-310-914A-253105
; Sequence 253105, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 253105
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-253105

Query Match 4.6%; Score 18.4; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       7038 CCCCTGAGCCCCAGACCAGC 7057
             ||||:|||||||||| |||||
Db          1 CCCCUGAGCCCCAGCCCAGC 20
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RESULT 3
US-10-310-914A-66019/c
; Sequence 66019, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66019
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-66019

Query Match 4.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       7057 CACTGACCAGGGGCCCTG 7074
             ||||||||||||||||||
Db         18 CACTGACCAGGGGCCCTG 1
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RESULT 4
US-10-310-914A-918753
; Sequence 918753, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01

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;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 918753
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-918753

  Query Match             4.2%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.4;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7189 ATCCCCCAAGCCCCAGA 7205
              |:||||||||||||||||
Db          2 AUCCCCCAAGCCCCAGA 18


Search completed: January 17, 2006, 15:04:33
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 14:51:12 ; Search time 1 Seconds
(without alignments)
1.451 Million cell updates/sec

Title: af287270
Perfect score: 401
Sequence: 1 GGGGTCTCAGCAGGGAACAA.....TAGCTCACTGCAGCCTCGAC 401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 101 seqs, 1809 residues

Total number of hits satisfying chosen parameters: 202

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 101 summaries

Database : af287270_copy_100_500.rge4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23.4	5.8	25	1	AX614112	ACCESSION:AX614112
	2	20.4	5.1	22	1	AR076805	ACCESSION:AR076805
	3	20.4	5.1	22	1	AR242947	ACCESSION:AR242947
	4	20.4	5.1	22	1	AR345130	ACCESSION:AR345130
	5	20.4	5.1	22	1	AX384999	ACCESSION:AX384999
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c	7	20	5.0	20	1	AR321577	ACCESSION:AR321577
	8	20	5.0	20	1	AR542568	ACCESSION:AR542568
c	9	19.4	4.8	21	1	AR345126	ACCESSION:AR345126
	10	19.4	4.8	21	1	AX741051	ACCESSION:AX741051
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	13	19	4.7	19	1	CS028508	ACCESSION:CS028508
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c	17	19	4.7	20	1	BD138317	ACCESSION:BD138317
	18	19	4.7	20	1	AR630295	ACCESSION:AR630295
	19	19	4.7	20	1	AR634606	ACCESSION:AR634606
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c	21	18.4	4.6	20	1	BD138315	ACCESSION:BD138315
c	22	18.4	4.6	20	1	BD138316	ACCESSION:BD138316
c	23	18.4	4.6	20	1	I31362	ACCESSION:I31362
c	24	18.4	4.6	20	1	AR232228	ACCESSION:AR232228
c	25	18.4	4.6	20	1	AR370243	ACCESSION:AR370243
c	26	18.2	4.5	19	1	AR074597	ACCESSION:AR074597
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c	28	18.2	4.5	19	1	I23816	ACCESSION:I23816
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ALIGNMENTS

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DEFINITION  Sequence 5137 from Patent WO02072882.
ACCESSION   AX614112
VERSION     AX614112.1  GI:28409541
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 5137 19-SEP-2002;
            OGHAM GmbH (DE)
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Db          1 GCTCTGTCGCCCAGGCTGGAGTGCA 25


RESULT 2
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LOCUS       AR076805                  22 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 2 from patent US 5959171.
ACCESSION   AR076805
VERSION     AR076805.1  GI:10003551
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hyttinen,J.-M., Korhonen,V.-P. and Janne,J.
  TITLE     Method for the production of biologically active polypeptides in a
            mammal's
  JOURNAL   Patent: US 5959171-A 2 28-SEP-1999;
FEATURES             Location/Qualifiers
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  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        464 GTGCAGTGGTGTGATCATAGCT 485
              |||||||||||||||| ||||
Db          1 GTGCAGTGGTGTGATCACAGCT 22


RESULT 3
AR242947
LOCUS       AR242947                  22 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 93 from patent US 6475739.
ACCESSION   AR242947
VERSION     AR242947.1  GI:27289609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Brunkow,M.E., Proll,S., Paeper,B. and Staehling-Hampton,K.
  TITLE     Methods for identifying genomic deletions
  JOURNAL   Patent: US 6475739-A 93 05-NOV-2002;
            Celltech R&D, Inc.; Bothell, WA
FEATURES             Location/Qualifiers
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  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 CAGGCTGGAGTGCAATGGTGTG 22


RESULT 4
AR345130
LOCUS       AR345130                  22 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6583112.
ACCESSION   AR345130
VERSION     AR345130.1  GI:33741766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Fu,Y.-H., Yu,C.-E., Oshima,J., Mulligan,J.T. and Schellenberg,G.D.
  TITLE     Gene products related to werner's syndrome
  JOURNAL   Patent: US 6583112-A 11 24-JUN-2003;
FEATURES             Location/Qualifiers
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  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        463 AGTGCAGTGGTGTGATCATAGC 484
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Db          1 AGTGCAGTGGTGTCATCATAGC 22


RESULT 5
AX384999
LOCUS       AX384999                  22 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 93 from Patent WO0210455.
ACCESSION   AX384999
VERSION     AX384999.1  GI:19578127
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brunkow,M.E., Proll,S. and Paeper,B.
  TITLE     Methods for identifying genomic deletions
  JOURNAL   Patent: WO 0210455-A 93 07-FEB-2002;
            Celltech R & D, Inc. (US) ; Straehling-Hampton, Karen (US)
FEATURES             Location/Qualifiers
     source          1. .22
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                     /note="PCR primer"

  Query Match             5.1%;  Score 20.4;  DB 1;  Length 22;
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  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        455 CAGGCTGGAGTGCAGTGGTGTG 476
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:49:05 ; Search time 736.68 Seconds
(without alignments)
1157.425 Million cell updates/sec

Title: US-10-754-446-6
Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_om:*
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6: gb_pat:*
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10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	1935	6	CQ750386	CQ750386 Sequence
	2	15	100.0	65347	14	AC130385	AC130385 Homo sapi
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	4	15	100.0	194763	14	AC150852	AC150852 Bos tauru
	5	15	100.0	216844	14	AC130788	AC130788 Bos tauru
c	6	15	100.0	218893	14	AC150547	AC150547 Bos tauru
	7	15	100.0	221544	14	AC127862	AC127862 Rattus no
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	9	15	100.0	235008	14	AC103239	AC103239 Rattus no
	10	15	100.0	239553	14	AC123201	AC123201 Rattus no
	11	15	100.0	246860	14	AC115225	AC115225 Rattus no
c	12	15	100.0	320746	14	AC128373	AC128373 Rattus no
	13	14	93.3	424	10	BV105141	BV105141 MARC 1149
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c	15	14	93.3	807	6	AX120670	AX120670 Sequence
c	16	14	93.3	930	6	AX064573	AX064573 Sequence
c	17	14	93.3	937	6	AX764219	AX764219 Sequence
	18	14	93.3	1323	6	AR547912	AR547912 Sequence
	19	14	93.3	1486	15	YSPADH	J01341 fisson yeas
	20	14	93.3	1985	15	AB000261	AB000261 Aspergill
	21	14	93.3	3369	15	AB000262	AB000262 Aspergill
	22	14	93.3	7319	6	AR227050	AR227050 Sequence
	23	14	93.3	9999	15	SPCC13B11	AL032681 S.pombe c
c	24	14	93.3	11304	1	AE012358	AE012358 Xanthomon
	25	14	93.3	12403	1	AE001706	AE001706 Thermotog
c	26	14	93.3	62398	14	AC166844	AC166844 Bos tauru
	27	14	93.3	69517	14	AC036117	AC036117 Homo sapi
c	28	14	93.3	69517	14	AC036117	AC036117 Homo sapi
c	29	14	93.3	79925	8	AC093719	AC093719 Homo sapi
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	33	14	93.3	110000	1	CP000050_19	Continuation (20 o
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	36	14	93.3	110000	15	AE017342_11	Continuation (12 o
	37	14	93.3	110000	15	AE017342_12	Continuation (13 o
c	38	14	93.3	110000	15	AE017348_02	Continuation (3 of
	39	14	93.3	116409	9	AC131118	AC131118 Mus muscu
c	40	14	93.3	139697	14	AC134207	AC134207 Rattus no
c	41	14	93.3	140176	8	AC022188	AC022188 Homo sapi
c	42	14	93.3	140219	9	AL603714	AL603714 Mouse DNA
	43	14	93.3	143509	14	AC068683	AC068683 Homo sapi
c	44	14	93.3	143733	14	AC152465	AC152465 Dasypus n
	45	14	93.3	155628	14	AC027810	AC027810 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS CQ750386 1935 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 36320 from Patent WO02068579.
ACCESSION CQ750386
VERSION CQ750386.1 GI:42381467
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 36320 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 15; DB 6; Length 1935;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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Db 912 CTGCCCACGGTACCT 926

RESULT 2
AC130385
LOCUS AC130385 65347 bp DNA linear HTG 10-OCT-2002
DEFINITION Homo sapiens chromosome 17 clone RP13-49B7 map 17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC130385

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VERSION     AC130385.4  GI:23683263
KEYWORDS    HTG; HTGS_PHASE0.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 65347)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP13-49B7
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 65347)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
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            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 65347)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 10, 2002 this sequence version replaced gi:23322704.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L27996
                Center clone name: 49_B_7
            --------------.
            * NOTE: This record contains 83 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      681: contig of 681 bp in length
            *      682      781: gap of 100 bp
            *      782     1477: contig of 696 bp in length
            *     1478     1577: gap of 100 bp
            *     1578     2269: contig of 692 bp in length
            *     2270     2369: gap of 100 bp
            *     2370     3056: contig of 687 bp in length
            *     3057     3156: gap of 100 bp
            *     3157     3835: contig of 679 bp in length
            *     3836     3935: gap of 100 bp
            *     3936     4629: contig of 694 bp in length
            *     4630     4729: gap of 100 bp
            *     4730     5426: contig of 697 bp in length
            *     5427     5526: gap of 100 bp
            *     5527     6218: contig of 692 bp in length
            *     6219     6318: gap of 100 bp
            *     6319     7003: contig of 685 bp in length
            *     7004     7103: gap of 100 bp
            *     7104     7798: contig of 695 bp in length
            *     7799     7898: gap of 100 bp
            *     7899     8584: contig of 686 bp in length
            *     8585     8684: gap of 100 bp
            *     8685     9370: contig of 686 bp in length
            *     9371     9470: gap of 100 bp
            *     9471    10159: contig of 689 bp in length
            *    10160    10259: gap of 100 bp
            *    10260    10954: contig of 695 bp in length
            *    10955    11054: gap of 100 bp
            *    11055    11740: contig of 686 bp in length
            *    11741    11840: gap of 100 bp
            *    11841    12487: contig of 647 bp in length
            *    12488    12587: gap of 100 bp
            *    12588    13282: contig of 695 bp in length
            *    13283    13382: gap of 100 bp
            *    13383    14069: contig of 687 bp in length
            *    14070    14169: gap of 100 bp
            *    14170    14855: contig of 686 bp in length
            *    14856    14955: gap of 100 bp
            *    14956    15633: contig of 678 bp in length
            *    15634    15733: gap of 100 bp
            *    15734    16426: contig of 693 bp in length
            *    16427    16526: gap of 100 bp
            *    16527    17198: contig of 672 bp in length
            *    17199    17298: gap of 100 bp
            *    17299    17983: contig of 685 bp in length
            *    17984    18083: gap of 100 bp
            *    18084    18777: contig of 694 bp in length
            *    18778    18877: gap of 100 bp
            *    18878    19548: contig of 671 bp in length
            *    19549    19648: gap of 100 bp
            *    19649    20345: contig of 697 bp in length
            *    20346    20445: gap of 100 bp
            *    20446    21138: contig of 693 bp in length
            *    21139    21238: gap of 100 bp
            *    21239    21942: contig of 704 bp in length
            *    21943    22042: gap of 100 bp
            *    22043    22751: contig of 709 bp in length
            *    22752    22851: gap of 100 bp
            *    22852    23545: contig of 694 bp in length
            *    23546    23645: gap of 100 bp
            *    23646    24330: contig of 685 bp in length
            *    24331    24430: gap of 100 bp
            *    24431    25092: contig of 662 bp in length
            *    25093    25192: gap of 100 bp
            *    25193    25893: contig of 701 bp in length
            *    25894    25993: gap of 100 bp
            *    25994    26679: contig of 686 bp in length
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 1677.48 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-6
Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	332	2	BF353711	QV2-HT069
	2	15	100.0	398	6	CB707082	CB707082 AMGNNUC:N
	3	15	100.0	615	6	CB579676	CB579676 AMGNNUC:N
	4	15	100.0	674	10	CG897726	CG897726 pastbac05
c	5	15	100.0	680	7	CK845557	CK845557 UI-R-BJ1-
c	6	15	100.0	696	8	DN105468	DN105468 1101440 M
c	7	15	100.0	697	8	CV796826	CV796826 UI-R-EB1-
	8	15	100.0	748	7	CO565750	CO565750 AGENCOURT
c	9	15	100.0	763	8	CV991014	CV991014 IpCGFr1_5
c	10	15	100.0	905	7	CN248276	CN248276 EST014180
	11	14	93.3	198	7	CO261528	CO261528 4133787 B
c	12	14	93.3	303	2	BF394984	BF394984 UI-R-CM0-
	13	14	93.3	303	9	AQ918623	AQ918623 RPCI-23-2
	14	14	93.3	318	8	DN278032	DN278032 1157316 M
	15	14	93.3	346	1	AW710109	AW710109 e1c09ne.f
c	16	14	93.3	373	5	BU994782	BU994782 HM08C24r
	17	14	93.3	405	2	BI187267	BI187267 a1g04fs.r
	18	14	93.3	445	1	AU007564	AU007564 AU007564
c	19	14	93.3	451	6	CF192358	CF192358 l4d08j2.f
	20	14	93.3	458	3	BI679825	BI679825 457072 MA
	21	14	93.3	461	1	AW358990	AW358990 44588 MAR
c	22	14	93.3	475	1	AW342926	AW342926 fj80g10.y
c	23	14	93.3	477	6	CF708620	CF708620 CCAAN62TF
	24	14	93.3	479	1	AU008740	AU008740 AU008740
	25	14	93.3	492	3	BI538165	BI538165 428581 MA
	26	14	93.3	514	3	BI899044	BI899044 480902 MA
	27	14	93.3	515	6	CF364476	CF364476 834426 MA
	28	14	93.3	519	2	BE235591	BE235591 143133 MA
	29	14	93.3	526	10	CE455507	CE455507 tigr-gss-
	30	14	93.3	528	1	AV434883	AV434883 AV434883
	31	14	93.3	529	2	BE013702	BE013702 125152 MA
	32	14	93.3	547	3	BI343534	BI343534 371728 MA
	33	14	93.3	548	1	AV439442	AV439442 AV439442
	34	14	93.3	549	2	BF198928	BF198928 248929 MA
	35	14	93.3	551	9	AZ840147	AZ840147 2M0136M01
c	36	14	93.3	552	6	CF673281	CF673281 STR01178
	37	14	93.3	554	1	AV665471	AV665471 AV665471
	38	14	93.3	578	3	BI774227	BI774227 466259 MA
	39	14	93.3	583	5	BX670522	BX670522 BX670522
	40	14	93.3	599	6	CB459576	CB459576 719362 MA
c	41	14	93.3	621	8	CX804839	CX804839 JGI_CAAJ1
c	42	14	93.3	630	6	CB461236	CB461236 721186 MA
	43	14	93.3	633	10	CW101525	CW101525 104_469_1
	44	14	93.3	637	8	DN128186	DN128186 1142243 M
	45	14	93.3	648	8	DN746616	DN746616 GL-Cf-340

ALIGNMENTS

RESULT 1
BF353711
LOCUS BF353711 332 bp mRNA linear EST 22-NOV-2000
DEFINITION QV2-HT0698-110700-267-a01 HT0698 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF353711
VERSION BF353711.1 GI:11312785
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 332)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-HT0698-110700-267-a01&t3=2000-07-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 331.
FEATURES Location/Qualifiers
source 1. .332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0698"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 15; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCCCACGGTACCT 15
||||||||||||||||
Db 236 CTGCCCACGGTACCT 250

RESULT 2
CB707082
LOCUS CB707082 398 bp mRNA linear EST 10-APR-2003
DEFINITION AMGNNUC:NRHY5-00217-H7-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhy5-00217-h7 5', mRNA sequence.
ACCESSION CB707082
VERSION CB707082.1 GI:29764230
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 398)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00217 row: h column: 7.
FEATURES Location/Qualifiers
source 1. .398
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy5-00217-h7"
/clone_lib="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W Rat hypothalamus adult female Wistar rat avg. Insert size 2.3 kb fraction 6 and 7"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCCCACGGTACCT 15
||||||||||||||||
Db 40 CTGCCCACGGTACCT 54

RESULT 3
CB579676
LOCUS CB579676 615 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:NRHY5-00106-F3-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhy5-00106-f3 5', mRNA sequence.
ACCESSION CB579676
VERSION CB579676.1 GI:29523717
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 615)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00106 row: f column: 3.
FEATURES Location/Qualifiers
source 1. .615
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy5-00106-f3"
/clone_lib="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W Rat hypothalamus adult female Wistar rat avg. Insert size 2.3 kb fraction 6 and 7"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCCCACGGTACCT 15
||||||||||||||||
Db 145 CTGCCCACGGTACCT 159

RESULT 4
CG897726
LOCUS CG897726 674 bp DNA linear GSS 08-DEC-2003
DEFINITION pastbac058xk02.b1.ab1 Res147 1 Pasteuria penetrans genomic 5', genomic survey sequence.
ACCESSION CG897726
VERSION CG897726.1 GI:39553221
KEYWORDS GSS.
SOURCE Pasteuria penetrans
ORGANISM Pasteuria penetrans
Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae; Pasteuria.
REFERENCE 1 (bases 1 to 674)
AUTHORS Opperman,C.H., Davies,K.G., Sosinski,B.R., Waterman,J. and Burke,M.
TITLE Unpublished Data
JOURNAL Unpublished (2003)
COMMENT Contact: Opperman CH
Center for the Biology of Nematode Parasitism and Nematode Interactions Unit
North Carolina State University and Rothamsted Research, Ltd.
Box 7253, NCSU, Raleigh, NC 27606, USA
Email: warthog@unity.ncsu.edu
Homology: e-val = 1e-51. Description = DNA ligase (Polydeoxyribonucleotide synthase [NAD+]) gi|3688229|emb|CAA09732.1| DNA ligase [Geobacillus stearothermophilus] Homology: e-val = 1e-50. Description = DNA ligase (polydeoxyribonucleotide synthase (NAD+)) [Bacillus halodurans] gi|15213980|sp|Q9KF37|DNLJ_BACHD DNA ligase (Polydeoxyribonucleotide synthase [NAD+]) gi|25293998|pir|A83731 DNA ligase (polydeoxyribonucleotide synthase (NAD+)) lig [imported] - row: k column: 2
Class: shotgun
High quality sequence stop: 674.
FEATURES Location/Qualifiers
source 1. .674
/organism="Pasteuria penetrans"
/mol_type="genomic DNA"
/strain="Res147"
/db_xref="taxon:86005"
/clone_lib="Res147 1"

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 674;

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 203.52 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-6
Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	14	AEB28962	Aeb28961 Human MCO
	2	14	93.3	560	13	ADQ49258	Adq49258 Novel can
c	3	14	93.3	807	5	AAH65551	Aah65551 C glutami
c	4	14	93.3	930	4	AAF72180	Aaf72180 Corynebac
c	5	14	93.3	937	10	ADD13464	Add13464 C. glutam
	6	14	93.3	1050	13	ADT47984	Adt47984 Bacterial
	7	14	93.3	1365	10	ADC81562	Adc81562 Recombina
	8	14	93.3	1422	13	ADS48605	Ads48605 Bacterial
c	9	14	93.3	1524	13	ADS56578	Ads56578 Bacterial
	10	14	93.3	349980	5	AAH68525	Aah68525 C glutami
	11	13.4	89.3	16	14	AEB28961	Aeb28961 Human MCO
c	12	13.4	89.3	118	5	ABV43024	Abv43024 Human pro
c	13	13.4	89.3	118	5	ABV34163	Abv34163 Human pro
	14	13.4	89.3	146	12	ACH93483	Ach93483 Human gen
c	15	13.4	89.3	252	12	ADP61947	Adp61947 Maize car
c	16	13.4	89.3	265	12	ADP61965	Adp61965 Maize car
c	17	13.4	89.3	267	12	ADP61934	Adp61934 Maize car
c	18	13.4	89.3	270	12	ADP61924	Adp61924 Maize car
c	19	13.4	89.3	272	12	ADP61945	Adp61945 Maize car
c	20	13.4	89.3	273	2	AAV09248	Aav09248 Human cyt
c	21	13.4	89.3	273	2	AAV12206	Aav12206 Human ret
c	22	13.4	89.3	273	6	AAD24507	Aad24507 Human P45
c	23	13.4	89.3	273	13	ADU66854	Adu66854 hP450RAI
c	24	13.4	89.3	273	14	ADV90794	Adv90794 Human ret
c	25	13.4	89.3	273	14	ADY62611	Ady62611 Human P45
c	26	13.4	89.3	274	2	AAV09249	Aav09249 Murine cy
c	27	13.4	89.3	274	2	AAV12207	Aav12207 Mouse ret
c	28	13.4	89.3	274	6	AAD24508	Aad24508 Mouse P45
c	29	13.4	89.3	274	13	ADU66855	Adu66855 mP450RAI
c	30	13.4	89.3	274	14	ADV90795	Adv90795 Murine re
c	31	13.4	89.3	274	14	ADY62612	Ady62612 Mouse P45
c	32	13.4	89.3	278	12	ADP61931	Adp61931 Maize car
c	33	13.4	89.3	285	12	ADP61916	Adp61916 Maize car
c	34	13.4	89.3	296	12	ADP61894	Adp61894 Maize car
c	35	13.4	89.3	298	4	AAL11859	Aal11859 Human bre
c	36	13.4	89.3	304	12	ADP61910	Adp61910 Maize car
c	37	13.4	89.3	311	12	ADP61878	Adp61878 Maize car
c	38	13.4	89.3	312	12	ADP61883	Adp61883 Maize car
c	39	13.4	89.3	314	12	ADP61875	Adp61875 Maize car
c	40	13.4	89.3	315	12	ADP61873	Adp61873 Maize car
c	41	13.4	89.3	321	12	ADP61869	Adp61869 Maize car
c	42	13.4	89.3	324	12	ADP61867	Adp61867 Maize car
c	43	13.4	89.3	341	4	AAS35653	Aas35653 Human car
c	44	13.4	89.3	341	10	ADE45732	Ade45732 Human car
c	45	13.4	89.3	341	13	ADJ07150	Adj07150 Human car

ALIGNMENTS

RESULT 1
AEB28962
ID AEB28962 standard; DNA; 15 BP.
XX
AC AEB28962;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene probe IVS MUT SEQ ID NO:6.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 3; SEQ ID NO 6; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a probe for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 15 BP; 2 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCCCACGGTACCT 15
||||||||||||||||
Db 1 CTGCCCACGGTACCT 15

RESULT 2
ADQ49258
ID ADQ49258 standard; DNA; 560 BP.
XX
AC ADQ49258;
XX
DT 21-OCT-2004 (first entry)
XX
DE Novel canine microarray-related DNA sequence SeqID560.
XX
KW canine microarray; drug screening; toxicity assay;
KW environmental pollutant; cellular response; gene expression profile;
KW toxic response; liver necrosis; fatty liver disease;
KW protein adduct formation; hepatitis; dog; ds.
XX
OS Canis familiaris.
XX
PN WO2004063324-A2.
XX
PD 29-JUL-2004.
XX
PF 05-MAY-2003; 2003WO-US013853.
XX
PR 03-MAY-2002; 2002US-0377240P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
XX
PI Diggans JC, Porter M, Wei T;
XX
DR WPI; 2004-561890/54.
XX
PT New isolated nucleic acid molecule, useful for drug screening and
PT toxicity assays or for assessing the impact, including toxicity, of a
PT compound, pharmaceutical agent or environmental pollutant on a cell or
PT living organism.
XX
PS Claim 1; SEQ ID NO 560; 41pp; English.
XX
CC This invention is related to a novel isolated canine nucleic acid
CC sequences and the construction of canine microarrays containing a
CC significant portion of the canine genome. The isolated canine nucleic
CC acid sequences of the invention may be useful for drug screening and
CC toxicity assays. The invention is therefore useful for assessing the
CC impact, including toxicity, of a compound, pharmaceutical agent or
CC environmental pollutant on a cell or living organism. The methods are
CC useful for detecting genes that are up- or down-regulated in canines in a
CC disease state. The sequences are useful as diagnostic agents or markers
CC to detect a cellular response in a sample individually or as part of a
CC gene expression profile. It is also useful as a target for agents that
CC modulate gene expression or activity. The database is useful for
CC producing electronic Northerns that allow the user to determine the cell
CC type or tissue in which a given gene is expressed and to allow
CC determination of the abundance or expression level of a given gene in a
CC particular tissue or cell. The methods are useful for determining the
CC similarity of a toxic response to one or more individual compounds. The
CC methods are useful for predicting at least one toxic response or the
CC likelihood that a compound or test agent will induce various specific
CC pathologies such as those of the liver (liver necrosis, fatty liver
CC disease, protein adduct formation or hepatitis), those of the kidney,
CC heart, brain or testes, or other pathologies associated with at least one
CC of the toxins. The methods are also useful for predicting or elucidating
CC the potential cellular pathways influenced, induced or modulated by the
CC compound or test agent due to the similarity of the expression profile
CC compared to the profile induced by a known toxin. The present sequence is
CC that of a canine DNA sequence which was claimed for use during the
CC production of a canine microarray of the invention.
XX
SQ Sequence 560 BP; 133 A; 168 C; 152 G; 102 T; 0 U; 5 Other;

Query Match 93.3%; Score 14; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCCCACGGTACC 14
||||||||||||||
Db 61 CTGCCCACGGTACC 74

RESULT 3
AAH65551/c
ID AAH65551 standard; DNA; 807 BP.
XX
AC AAH65551;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 586.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG90332.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 586; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 362.28 Seconds
(without alignments)
342.389 Million cell updates/sec

Title: US-10-754-446-6
Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	14	93.3	25	8	US-10-719-900-215409	Sequence 215409,
c 3	14	93.3	491	7	US-10-424-599-52366	Sequence 52366, A
c 4	14	93.3	500	4	US-09-925-065A-757224	Sequence 757224,
c 5	14	93.3	807	3	US-09-738-626-586	Sequence 586, App
c 6	14	93.3	937	8	US-10-494-675-31	Sequence 31, Appl
7	14	93.3	1050	6	US-10-369-493-46422	Sequence 46422, A
8	14	93.3	1365	6	US-10-372-473-8	Sequence 8, Appli
9	14	93.3	1422	6	US-10-369-493-27035	Sequence 27035, A
c 10	14	93.3	1524	6	US-10-369-493-32252	Sequence 32252, A
11	14	93.3	7319	5	US-10-194-163-510	Sequence 510, App
12	14	93.3	3309400	3	US-09-738-626-1	Sequence 1, Appli
13	13.4	89.3	16	9	US-10-754-446-5	Sequence 5, Appli
c 14	13.4	89.3	25	10	US-11-036-317-515390	Sequence 515390,
c 15	13.4	89.3	118	8	US-10-357-930-34181	Sequence 34181, A
c 16	13.4	89.3	118	8	US-10-357-930-43043	Sequence 43043, A
17	13.4	89.3	146	6	US-10-029-386-26678	Sequence 26678, A
18	13.4	89.3	201	8	US-10-719-993-9298	Sequence 9298, Ap
c 19	13.4	89.3	201	8	US-10-741-600-14149	Sequence 14149, A
c 20	13.4	89.3	201	8	US-10-741-600-14194	Sequence 14194, A
c 21	13.4	89.3	201	8	US-10-741-600-14264	Sequence 14264, A
c 22	13.4	89.3	201	8	US-10-741-600-14300	Sequence 14300, A
c 23	13.4	89.3	201	8	US-10-741-600-14338	Sequence 14338, A
c 24	13.4	89.3	201	8	US-10-741-600-14361	Sequence 14361, A
c 25	13.4	89.3	201	8	US-10-741-600-26703	Sequence 26703, A
c 26	13.4	89.3	201	8	US-10-741-600-49737	Sequence 49737, A
c 27	13.4	89.3	252	3	US-09-987-899-5016	Sequence 5016, Ap
c 28	13.4	89.3	265	3	US-09-987-899-5034	Sequence 5034, Ap
c 29	13.4	89.3	267	3	US-09-987-899-5003	Sequence 5003, Ap
c 30	13.4	89.3	270	3	US-09-987-899-4993	Sequence 4993, Ap
c 31	13.4	89.3	272	3	US-09-987-899-5014	Sequence 5014, Ap
c 32	13.4	89.3	273	8	US-10-855-595-33	Sequence 33, Appl
c 33	13.4	89.3	273	8	US-10-855-532-33	Sequence 33, Appl
c 34	13.4	89.3	274	8	US-10-855-595-34	Sequence 34, Appl
c 35	13.4	89.3	274	8	US-10-855-532-34	Sequence 34, Appl
c 36	13.4	89.3	278	3	US-09-987-899-5000	Sequence 5000, Ap
c 37	13.4	89.3	285	3	US-09-987-899-4985	Sequence 4985, Ap
c 38	13.4	89.3	296	3	US-09-987-899-4963	Sequence 4963, Ap
c 39	13.4	89.3	304	3	US-09-987-899-4979	Sequence 4979, Ap
c 40	13.4	89.3	310	7	US-10-242-535A-32082	Sequence 32082, A
c 41	13.4	89.3	310	7	US-10-085-783A-32082	Sequence 32082, A
c 42	13.4	89.3	311	3	US-09-987-899-4947	Sequence 4947, Ap
c 43	13.4	89.3	312	3	US-09-796-692-3501	Sequence 3501, Ap
c 44	13.4	89.3	312	3	US-09-987-899-4952	Sequence 4952, Ap
c 45	13.4	89.3	312	5	US-10-040-862-3501	Sequence 3501, Ap

ALIGNMENTS

RESULT 1
US-10-754-446-6
; Sequence 6, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-754-446-6

Query Match 100.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 CTGCCCACGGTACCT 15
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RESULT 2
US-10-719-900-215409
; Sequence 215409, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 215409

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;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-215409

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Qy          2 TGCCCACGGTACCT 15
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Db          3 TGCCCACGGTACCT 16


RESULT 3
US-10-424-599-52366/c
; Sequence 52366, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 52366
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_182C.1
US-10-424-599-52366

  Query Match             93.3%;  Score 14;  DB 7;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCCACGGTACCT 15
              ||||||||||||||
Db        190 TGCCCACGGTACCT 177


RESULT 4
US-09-925-065A-757224/c
; Sequence 757224, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 757224
;   LENGTH: 500
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-757224

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACC 14
              ||||||||||||||
Db        119 CTGCCCACGGTACC 106


RESULT 5
US-09-738-626-586/c
; Sequence 586, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 586
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-586

  Query Match             93.3%;  Score 14;  DB 3;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCCACGGTACCT 15
              ||||||||||||||
Db        145 TGCCCACGGTACCT 132


RESULT 6
US-10-494-675-31/c
; Sequence 31, Application US/10494675
; Publication No. US20050019877A1
; GENERAL INFORMATION:
;  APPLICANT: Zelder, Oskar
;  APPLICANT:  Pompejus, Markus
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Klopprogge, Corinna
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: Genes coding for metabolic pathway proteins
;  FILE REFERENCE: BGI-163US
;  CURRENT APPLICATION NUMBER: US/10/494,675
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: PCT/EP02/12141
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: DE 101 54 292.1
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 164
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:59:57 ; Search time 184.56 Seconds
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Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

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Searched: 6038814 seqs, 404674181 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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c	2	13.4	89.3	201	6	US-10-995-561-41220	Sequence 41220, A
c	3	13.4	89.3	708	6	US-10-750-185-33670	Sequence 33670, A
c	4	13.4	89.3	708	6	US-10-750-623-33670	Sequence 33670, A
c	5	13.4	89.3	847	6	US-10-750-185-61862	Sequence 61862, A
c	6	13.4	89.3	847	6	US-10-750-623-61862	Sequence 61862, A
c	7	13.4	89.3	1372	6	US-10-750-185-57181	Sequence 57181, A
c	8	13.4	89.3	1372	6	US-10-750-623-57181	Sequence 57181, A
c	9	13.4	89.3	1404	6	US-10-517-939-303	Sequence 303, App
c	10	13.4	89.3	9471	6	US-10-821-234-410	Sequence 410, App
	11	13.4	89.3	168516	7	US-11-121-086-3	Sequence 3, Appli
c	12	13.4	89.3	1125000	6	US-10-995-561-13286	Sequence 13286, A
	13	13	86.7	93	6	US-10-310-914A-17319	Sequence 17319, A
c	14	13	86.7	441	6	US-10-835-615-111	Sequence 111, App
c	15	13	86.7	3336	6	US-10-750-185-55139	Sequence 55139, A
c	16	13	86.7	3336	6	US-10-750-623-55139	Sequence 55139, A
	17	13	86.7	167116	7	US-11-121-086-44	Sequence 44, Appl
	18	13	86.7	182303	7	US-11-121-086-45	Sequence 45, Appl
	19	12.4	82.7	19	8	US-11-101-244-511715	Sequence 511715,
c	20	12.4	82.7	19	8	US-11-101-244-1350721	Sequence 1350721,
	21	12.4	82.7	19	9	US-11-083-784-511715	Sequence 511715,
c	22	12.4	82.7	19	9	US-11-083-784-1350721	Sequence 1350721,
c	23	12.4	82.7	20	6	US-10-310-914A-1021148	Sequence 1021148,
c	24	12.4	82.7	22	6	US-10-310-914A-1387393	Sequence 1387393,
	25	12.4	82.7	25	6	US-10-310-914A-855540	Sequence 855540,
c	26	12.4	82.7	25	7	US-11-121-849-221946	Sequence 221946,
	27	12.4	82.7	25	7	US-11-121-849-564915	Sequence 564915,
c	28	12.4	82.7	201	6	US-10-995-561-5198	Sequence 5198, Ap
c	29	12.4	82.7	201	6	US-10-995-561-5207	Sequence 5207, Ap
c	30	12.4	82.7	201	6	US-10-995-561-5283	Sequence 5283, Ap
c	31	12.4	82.7	201	6	US-10-995-561-5292	Sequence 5292, Ap
c	32	12.4	82.7	201	6	US-10-995-561-5362	Sequence 5362, Ap
c	33	12.4	82.7	201	6	US-10-995-561-5371	Sequence 5371, Ap
c	34	12.4	82.7	201	6	US-10-995-561-16810	Sequence 16810, A
c	35	12.4	82.7	201	6	US-10-995-561-16812	Sequence 16812, A
c	36	12.4	82.7	201	6	US-10-995-561-24263	Sequence 24263, A
c	37	12.4	82.7	201	6	US-10-995-561-24481	Sequence 24481, A
c	38	12.4	82.7	201	6	US-10-995-561-28948	Sequence 28948, A
c	39	12.4	82.7	201	6	US-10-995-561-29048	Sequence 29048, A
c	40	12.4	82.7	201	6	US-10-995-561-29049	Sequence 29049, A
c	41	12.4	82.7	201	6	US-10-995-561-29168	Sequence 29168, A
	42	12.4	82.7	600	7	US-11-128-061-4350	Sequence 4350, Ap
c	43	12.4	82.7	625	6	US-10-750-185-54379	Sequence 54379, A
c	44	12.4	82.7	625	6	US-10-750-623-54379	Sequence 54379, A
	45	12.4	82.7	1059	6	US-10-750-185-44993	Sequence 44993, A

ALIGNMENTS

RESULT 1
US-11-055-822-855/c
; Sequence 855, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 855
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(907)
; OTHER INFORMATION: RXN00708
US-11-055-822-855

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  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        245 TGCCCACGGTACCT 232


RESULT 2
US-10-995-561-41220/c
; Sequence 41220, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41220
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-41220

  Query Match             89.3%;  Score 13.4;  DB 6;  Length 201;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACCT 15
              |||||||||| ||||
Db         42 CTGCCCACGGGACCT 28


RESULT 3
US-10-750-185-33670/c
; Sequence 33670, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33670
;   LENGTH: 708
;   TYPE: DNA
;   ORGANISM: Bovine  19866880906011
US-10-750-185-33670

  Query Match             89.3%;  Score 13.4;  DB 6;  Length 708;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACCT 15
              ||||||| |||||||
Db        106 CTGCCCAGGGTACCT 92


RESULT 4
US-10-750-623-33670/c
; Sequence 33670, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33670
;   LENGTH: 708
;   TYPE: DNA
;   ORGANISM: Bovine  19866880906011
US-10-750-623-33670

  Query Match             89.3%;  Score 13.4;  DB 6;  Length 708;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACCT 15
              ||||||| |||||||
Db        106 CTGCCCAGGGTACCT 92


RESULT 5
US-10-750-185-61862/c
; Sequence 61862, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61862
;   LENGTH: 847
;   TYPE: DNA
;   ORGANISM: Bovine  19866881794277
US-10-750-185-61862

  Query Match             89.3%;  Score 13.4;  DB 6;  Length 847;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACCT 15
              |||||||||| ||||
Db        177 CTGCCCACGGGACCT 163


RESULT 6
US-10-750-623-61862/c
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:32:47 ; Search time 54.6 Seconds
(without alignments)
488.341 Million cell updates/sec

Title: US-10-754-446-6
Perfect score: 15
Sequence: 1 ctgcccacggtacct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query % Match	Length	DB	ID	Description
	1	14	93.3	1323	3	US-09-248-796A-3043	Sequence 3043, Ap
	2	14	93.3	7319	3	US-09-221-017B-510	Sequence 510, App
	3	13.4	89.3	63	2	US-08-707-237A-5	Sequence 5, Appli
c	4	13.4	89.3	273	3	US-08-882-164D-33	Sequence 33, Appl
c	5	13.4	89.3	273	3	US-09-668-482-33	Sequence 33, Appl
c	6	13.4	89.3	274	3	US-08-882-164D-34	Sequence 34, Appl
c	7	13.4	89.3	274	3	US-09-668-482-34	Sequence 34, Appl
	8	13.4	89.3	482	3	US-10-131-827-8312	Sequence 8312, Ap
c	9	13.4	89.3	601	3	US-09-949-016-78826	Sequence 78826, A
c	10	13.4	89.3	601	3	US-09-949-016-169541	Sequence 169541,
c	11	13.4	89.3	601	3	US-09-949-016-169542	Sequence 169542,
c	12	13.4	89.3	601	3	US-09-949-016-169543	Sequence 169543,
	13	13.4	89.3	1047	3	US-09-107-433-1277	Sequence 1277, Ap
c	14	13.4	89.3	1125	2	US-08-583-562B-9	Sequence 9, Appli
c	15	13.4	89.3	1125	2	US-08-779-113-9	Sequence 9, Appli
	16	13.4	89.3	1143	3	US-09-583-110-2113	Sequence 2113, Ap
c	17	13.4	89.3	1494	2	US-08-583-562B-11	Sequence 11, Appl
c	18	13.4	89.3	1494	2	US-08-779-113-11	Sequence 11, Appl
c	19	13.4	89.3	1533	3	US-09-075-454-11	Sequence 11, Appl
c	20	13.4	89.3	1660	3	US-09-347-650-11	Sequence 11, Appl
c	21	13.4	89.3	2574	2	US-08-583-562B-1	Sequence 1, Appli
c	22	13.4	89.3	2574	2	US-08-779-113-1	Sequence 1, Appli
c	23	13.4	89.3	2677	3	US-08-882-164D-36	Sequence 36, Appl
c	24	13.4	89.3	2677	3	US-09-668-482-36	Sequence 36, Appl
c	25	13.4	89.3	3252	3	US-09-774-528-104	Sequence 104, App
c	26	13.4	89.3	3252	3	US-10-120-988-104	Sequence 104, App
c	27	13.4	89.3	3561	2	US-08-097-997A-12	Sequence 12, Appl
c	28	13.4	89.3	3561	3	US-08-665-574C-12	Sequence 12, Appl
c	29	13.4	89.3	3561	3	US-08-946-994-12	Sequence 12, Appl
c	30	13.4	89.3	4080	3	US-09-016-434-1353	Sequence 1353, Ap
c	31	13.4	89.3	4176	3	US-09-972-800A-17	Sequence 17, Appl
c	32	13.4	89.3	4176	3	US-09-023-655-1378	Sequence 1378, Ap
	33	13.4	89.3	5238	3	US-09-620-312D-351	Sequence 351, App
c	34	13.4	89.3	7559	2	US-08-250-848-2	Sequence 2, Appli
	35	13.4	89.3	11915	3	US-08-961-527-96	Sequence 96, Appl
	36	13.4	89.3	12681	3	US-09-949-016-16576	Sequence 16576, A
	37	13.4	89.3	15353	3	US-09-949-016-13454	Sequence 13454, A
c	38	13.4	89.3	17478	3	US-09-949-016-12194	Sequence 12194, A
c	39	13.4	89.3	17479	3	US-09-949-016-13057	Sequence 13057, A
c	40	13.4	89.3	44821	3	US-09-949-016-13764	Sequence 13764, A
c	41	13.4	89.3	67745	3	US-09-949-016-17251	Sequence 17251, A
c	42	13.4	89.3	110585	3	US-09-949-016-13427	Sequence 13427, A
c	43	13.4	89.3	160759	3	US-09-949-016-16514	Sequence 16514, A
c	44	13.4	89.3	784019	3	US-09-949-016-14033	Sequence 14033, A
c	45	13.4	89.3	828152	3	US-09-949-016-12777	Sequence 12777, A

ALIGNMENTS

RESULT 1
US-09-248-796A-3043
; Sequence 3043, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3043
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3043

Query Match 93.3%; Score 14; DB 3; Length 1323;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGCCCACGGTACC 14
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Db       1025 CTGCCCACGGTACC 1038
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RESULT 2
US-09-221-017B-510
; Sequence 510, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows
;       SOFTWARE:  FastSEQ for Windows Version 2.0b
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/221,017B
;       FILING DATE:  23-DEC-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PP1182
;       FILING DATE:  31-DEC-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PP1546
;       FILING DATE:  30-JAN-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PP2911
;       FILING DATE:  09-APR-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/AU98/01023
;       FILING DATE:  10-DEC-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monroy, Gladys H
;       REGISTRATION NUMBER:  32,430
;       REFERENCE/DOCKET NUMBER:  27340-20021.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-813-5600
;       TELEFAX:  650-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  510:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7319 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  circular
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  UNKNOWN
;     ORIGINAL SOURCE:
;       ORGANISM:  PORYPHYROMONAS GINGIVALIS
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1...7319
US-09-221-017B-510

  Query Match             93.3%;  Score 14;  DB 3;  Length 7319;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCCCACGGTACC 14
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Db       3741 CTGCCCACGGTACC 3754


RESULT 3
US-08-707-237A-5
; Sequence 5, Application US/08707237A
; Patent No. 5830713
;  GENERAL INFORMATION:
;     APPLICANT:  Ferrari, Franco A.
;     APPLICANT:  Capello, Joseph
;     APPLICANT:  Crissman, John W.
;     APPLICANT:  Dorman, Mary A.
;     TITLE OF INVENTION:  METHODS FOR PREPARING SYNTHETIC
;     TITLE OF INVENTION:  REPETITIVE DNA
;     NUMBER OF SEQUENCES:  108
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;       STREET:  Four Embarcadero Center, Suite 3400
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  94111-4187
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/707,237A
;       FILING DATE:  03-SEP-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/175,155
;       FILING DATE:  29-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/053,049
;       FILING DATE:  22-APR-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/609,716
;       FILING DATE:  06-NOV-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/269,429
;       FILING DATE:  09-NOV-1988
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/114,618
;       FILING DATE:  29-OCT-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 06/927,258
;       FILING DATE:  04-NOV-1986
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Trecartin, Richard F.
;       REGISTRATION NUMBER:  31,801
;       REFERENCE/DOCKET NUMBER:  A-55186-10/WHD
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;       TELEX:  910 277299
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  63 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
US-08-707-237A-5

  Query Match             89.3%;  Score 13.4;  DB 2;  Length 63;
  Best Local Similarity   93.3%;  Pred. No. 5.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         26 CTACCCACGGTACCT 40


RESULT 4
US-08-882-164D-33/c
; Sequence 33, Application US/08882164D
; Patent No. 6306624
;  GENERAL INFORMATION:
;     APPLICANT:  Petkovich, P. Martin, White, Jay A.,
;     APPLICANT:  Beckett, Barbara R., Jones, Glenville
;     TITLE OF INVENTION:  Retinoid Metabolizing Protein
;     NUMBER OF SEQUENCES:  43
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Blake, Cassels & Graydon
;       STREET:  Box 25, Commerce Court West
;       CITY:  Toronto
;       STATE:  Ontario
;       COUNTRY:  Canada
;       ZIP:  M5L 1A9
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3 1/2 inch, 1.4 Mb storage
;       COMPUTER:  COMPAQ, IBM PC compatible
;       OPERATING SYSTEM:  MS-DOS 5.1
;       SOFTWARE:  WORD PERFECT
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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	16	100.0	659	10	BV230130	BV230130 S233P6354
c 4	16	100.0	661	10	G93242	G93242 S208P6433RE
5	16	100.0	728	10	BV524331	BV524331 G591P6065
c 6	16	100.0	925	10	BV526258	BV526258 G591P6047
7	16	100.0	1740	6	AX280021	AX280021 Sequence
8	16	100.0	1829	6	CQ719994	CQ719994 Sequence
9	16	100.0	2004	8	AF249319	AF249319 Homo sapi
10	16	100.0	2037	8	HSA293970	AJ293970 Homo sapi
11	16	100.0	2049	8	AK026102	AK026102 Homo sapi
12	16	100.0	2051	8	AF287269	AF287269 Homo sapi
13	16	100.0	2052	6	AX083508	AX083508 Sequence
14	16	100.0	2063	8	AK222673	AK222673 Homo sapi
15	16	100.0	2065	8	AB125179	AB125179 Macaca fa
16	16	100.0	2078	8	BC005149	BC005149 Homo sapi
17	16	100.0	2094	6	BD233734	BD233734 31 human
18	16	100.0	2095	6	AX280019	AX280019 Sequence
19	16	100.0	2272	8	HSA293659	AJ293659 Homo sapi
c 20	16	100.0	12300	1	AE005887	AE005887 Caulobact
21	16	100.0	13270	8	AF287270	AF287270 Homo sapi
22	16	100.0	47196	14	BX546462_4	Continuation (5 of
c 23	16	100.0	49264	14	AC164672	AC164672 Bos tauru
c 24	16	100.0	128501	8	AC012614	AC012614 Homo sapi
c 25	16	100.0	150909	9	AC116811	AC116811 Mus muscu
26	16	100.0	151130	9	AC127432	AC127432 Mus muscu
c 27	16	100.0	155645	14	AC021153	AC021153 Homo sapi
28	16	100.0	157952	8	AP003691	AP003691 Homo sapi
c 29	16	100.0	158063	8	AP001046	AP001046 Homo sapi
30	16	100.0	165994	9	AC129207	AC129207 Mus muscu
31	16	100.0	173081	9	AC159338	AC159338 Mus muscu
32	16	100.0	173126	8	AC008878	AC008878 Homo sapi
c 33	16	100.0	175177	9	AC124383	AC124383 Mus muscu
34	16	100.0	179556	14	AC018734	AC018734 Homo sapi
35	16	100.0	180770	14	AC153861	AC153861 Mus muscu
36	16	100.0	188593	8	AC016877	AC016877 Homo sapi
37	16	100.0	194042	9	AC153850	AC153850 Mus muscu
c 38	16	100.0	194364	14	AC164574	AC164574 Mus muscu
c 39	16	100.0	208898	14	AC164628	AC164628 Mus muscu
c 40	16	100.0	210408	8	AC010608	AC010608 Homo sapi
41	16	100.0	213826	9	AL845298	AL845298 Mouse DNA
42	16	100.0	222368	14	AC095138	AC095138 Rattus no
c 43	16	100.0	225535	14	AC111381	AC111381 Rattus no
c 44	16	100.0	232747	14	AC116259	AC116259 Rattus no
45	16	100.0	253693	14	AC131839	AC131839 Rattus no

ALIGNMENTS

RESULT 1
BV401493/c
LOCUS BV401493 536 bp DNA linear STS 01-FEB-2005
DEFINITION S229P6332RE8.T0 GermanShepherd Canis familiaris STS genomic, sequence tagged site.
ACCESSION BV401493
VERSION BV401493.1 GI:57775274
KEYWORDS STS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 536)
AUTHORS Lindblad-Toh,K.
TITLE The genome sequence of Canis familiaris
JOURNAL Unpublished (2004)
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 536
Protocol:
WGS-discovery (WGS):
Paired-end low-coverage whole genome shotgun reads were generated from 9 breeds
(German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador Retriever, English
Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese Water Dog -100,000 each)
and five other canids (Chinese, Alaskan, Indian and Spanish Gray Wolf as well as the
Californian Coyote).
The WGS reads were placed uniquely on the CanFam1.0 boxer assembly and SNP detection was

carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were
annotated with alleles from the boxer and the breed or canid from which the particular
read came. The validation rate for these SNPs was estimated at approximately 98%.
WGA-discovery (WGA) of Boxer/Poodle SNPs:
A second set of SNPs was generated using a similar methodology except that the contigs
from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this
sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned
before the poddle seqeunce was placed uniquely on the CanFam1.0 boxer assembly and SNP
detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the
boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.
Internal-WGA-discovery (I-WGA):
A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were
defined as mismatch positions that had a base quality of >= 30 on both reads in a region
that aligned without gaps, and with at most one additional mismatch in the ten flanking
bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were
annotated with alleles between the two boxer alleles. The validation rate for these SNPs
was estimated at approximately TBD%.

```
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="GermanShepherd"
                     /db_xref="taxon:9615"
                     /map="+ 8 22-462 74954487-74954047"
                     /clone_lib="GermanShepherd"
     STS             <1. .>536
ORIGIN

  Query Match             100.0%;  Score 16;  DB 10;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACAT 16
              ||||||||||||||||
Db        468 AGACCCAGGCCCACAT 453


RESULT 2
AF305572S5
LOCUS       AF305572S5               579 bp    DNA     linear   PRI 26-DEC-2000
DEFINITION  Homo sapiens mucolipin 1 (MCOLN1) gene, exons 6 and 7.
ACCESSION   AF305576
VERSION     AF305576.1  GI:11991202
KEYWORDS    .
SEGMENT     5 of 8
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
            Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
  TITLE     Identification of the gene causing mucolipidosis type IV
  JOURNAL   Nat. Genet. 26 (1), 118-123 (2000)
   PUBMED   10973263
REFERENCE   2  (bases 1 to 579)
  AUTHORS   Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
            Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute
            of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     exon            129. .225
                     /gene="MCOLN1"
                     /number=6
     exon            423. .522
                     /gene="MCOLN1"
                     /number=7
ORIGIN

  Query Match             100.0%;  Score 16;  DB 8;  Length 579;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACAT 16
              ||||||||||||||||
Db        472 AGACCCAGGCCCACAT 487


RESULT 3
BV230130/c
LOCUS       BV230130                 659 bp    DNA     linear   STS 19-JAN-2005
DEFINITION  S233P6354FD9.T0 LabradorRetriever Canis familiaris STS genomic,
            sequence tagged site.
ACCESSION   BV230130
VERSION     BV230130.1  GI:57292672
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   Lindblad-Toh,K.
  TITLE     The genome sequence of Canis familiaris
  JOURNAL   Unpublished (2004)
COMMENT
            Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: kersli@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 659
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).
            The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
            and SNP detection was
            carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
            485941 SNPs were
            annotated with alleles from the boxer and the breed or canid from
            which the particular
            read came. The validation rate for these SNPs was estimated at
            approximately 98%.
            WGA-discovery (WGA) of Boxer/Poodle SNPs:
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 1789.31 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-7
Perfect score: 16
Sequence: 1 agacccaggcccacat 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	278	9	AZ491094	AZ491094 1M0324P22
	2	16	100.0	291	8	T29948	T29948 EST100452 H
	3	16	100.0	316	8	F07345	F07345 HSC22G041 n
	4	16	100.0	324	1	AW486159	AW486159 71019 MAR
	5	16	100.0	331	8	Z43611	Z43611 HSC1GD031 n
	6	16	100.0	333	8	T35364	T35364 EST83466 Hu
	7	16	100.0	350	8	Z43604	Z43604 HSC1GA071 n
	8	16	100.0	371	1	AW356454	AW356454 38818 MAR
	9	16	100.0	387	1	AW425724	AW425724 58155 MAR
	10	16	100.0	387	2	BE478501	BE478501 162788 BA
c	11	16	100.0	404	9	AZ847535	AZ847535 2M0148I08
	12	16	100.0	442	1	AW785343	AW785343 116302 MA
	13	16	100.0	466	9	AZ073212	AZ073212 RPCI-23-3
	14	16	100.0	478	2	BG383183	BG383183 301136 MA
	15	16	100.0	500	2	BF443224	BF443224 260639 MA
c	16	16	100.0	510	6	CA889269	CA889269 B0151H02-
c	17	16	100.0	540	7	CJ017244	CJ017244 CJ017244
	18	16	100.0	578	9	AZ286475	AZ286475 RPCI-23-4
	19	16	100.0	593	7	CN788730	CN788730 4123095 B
	20	16	100.0	740	6	CA489568	CA489568 AGENCOURT
	21	16	100.0	772	7	CK465307	CK465307 936399 MA
	22	16	100.0	775	10	CG740895	CG740895 ZMMBBc018
c	23	16	100.0	777	7	CK467406	CK467406 938703 MA
	24	16	100.0	779	7	CK468501	CK468501 939896 MA
c	25	16	100.0	817	2	BI252802	BI252802 602952877
	26	16	100.0	826	2	BG913075	BG913075 602806464
c	27	16	100.0	845	2	BG176074	BG176074 602337904
c	28	16	100.0	862	7	CK469557	CK469557 AGENCOURT
	29	16	100.0	868	3	BI909885	BI909885 603070517
	30	16	100.0	872	10	CZ363216	CZ363216 ZMMBF0141
	31	16	100.0	873	6	CD558014	CD558014 AGENCOURT
	32	16	100.0	878	5	BQ956452	BQ956452 AGENCOURT
c	33	16	100.0	901	5	BX433310	BX433310 BX433310
c	34	16	100.0	961	10	CZ363668	CZ363668 ZMMBF0142
	35	16	100.0	979	5	BQ918296	BQ918296 AGENCOURT
	36	16	100.0	993	2	BG739714	BG739714 602630410
	37	16	100.0	1056	11	CNS037W4	AL231853 Tetraodon
	38	16	100.0	1078	5	BX362786	BX362786 BX362786
	39	16	100.0	1273	4	CR616477	CR616477 full-leng
	40	16	100.0	1712	10	AY410284	AY410284 Pan trogl
	41	16	100.0	1743	10	AY410283	AY410283 Homo sapi
	42	16	100.0	1996	4	CR622331	CR622331 full-leng
	43	16	100.0	2108	4	AK052519	AK052519 Mus muscu
	44	15.6	97.5	961	5	BX397924	BX397924 BX397924
	45	15.2	95.0	1026	5	BX364018	BX364018 BX364018

ALIGNMENTS

RESULT 1
AZ491094
LOCUS AZ491094 278 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0324P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0324P22 F, genomic survey sequence.
ACCESSION AZ491094
VERSION AZ491094.1 GI:10662462
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 278)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0324 row: P column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 278.
FEATURES Location/Qualifiers
source 1. .278
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0324P22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGACCCAGGCCCACAT 16
              ||||||||||||||||
Db        129 AGACCCAGGCCCACAT 144
```

RESULT 2
T29948
LOCUS T29948 291 bp mRNA linear EST 06-SEP-1995
DEFINITION EST100452 Human Pancreas Homo sapiens cDNA 5' end similar to None, mRNA sequence.
ACCESSION T29948
VERSION T29948.1 GI:612046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 291)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
PUBMED 7566098
COMMENT Other_ESTs: THC11326
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .291
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):107961"
/db_xref="taxon:9606"
/clone_lib="Human Pancreas"
/note="Organ: pancreas"
ORIGIN

Query Match 100.0%; Score 16; DB 8; Length 291;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGACCCAGGCCCACAT 16
              ||||||||||||||||
Db        186 AGACCCAGGCCCACAT 201
```

RESULT 3
F07345
LOCUS F07345 316 bp mRNA linear EST 20-FEB-1995
DEFINITION HSC22G041 normalized infant brain cDNA Homo sapiens cDNA clone c-22g04, mRNA sequence.
ACCESSION F07345
VERSION F07345.1 GI:672999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 316)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
PUBMED 7757816
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-22g04
Seq primer: (-21)M13_universal.
FEATURES Location/Qualifiers
source 1. .316
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-22g04"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
ORIGIN

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 217.088 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-7
Perfect score: 16
Sequence: 1 agacccaggcccacat 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	16	14	AEB28963	Aeb28963 Human MCO
c	2	16	100.0	1619	4	AAI61022	Aai61022 Human pol
	3	16	100.0	1740	6	AAI71700	Aai71700 Human TRP
	4	16	100.0	1740	6	ABL40755	Abl40755 Human TLC
	5	16	100.0	1741	4	AAI59236	Aai59236 Human pol
	6	16	100.0	1743	9	ADB84284	Adb84284 Human muc
	7	16	100.0	1743	14	ADV66231	Adv66231 TRP-like
	8	16	100.0	2051	13	ADP25150	Adp25150 PRO polyp
	9	16	100.0	2052	4	AAF81753	Aaf81753 Human mem
	10	16	100.0	2092	5	AAS72274	Aas72274 DNA encod
	11	16	100.0	2092	6	ABL90358	Abl90358 Human pol
	12	16	100.0	2094	3	AAA39067	Aaa39067 Human sec
	13	16	100.0	2095	6	AAI71699	Aai71699 Human TRP
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	16	16	100.0	2140	12	ADQ24925	Adq24925 Human sof
	17	16	100.0	11365	4	AAK73827	Aak73827 Human imm
	18	16	100.0	13270	9	ADB84283	Adb84283 Human muc
	19	16	100.0	20046	4	AAK73826	Aak73826 Human imm
	20	16	100.0	340449	8	AAL52198	Aal52198 Human sec
c	21	15	93.8	384	6	ABN15902	Abn15902 Human ORF
c	22	15	93.8	449	11	ADT97636	Adt97636 Colon can
c	23	15	93.8	449	11	ADX44118	Adx44118 Human cDN
	24	15	93.8	471	13	ADU10604	Adu10604 Solid tum
	25	15	93.8	502	4	AAK61151	Aak61151 Human imm
c	26	15	93.8	514	13	ADQ49858	Adq49858 Novel can
c	27	15	93.8	625	4	AAH05091	Aah05091 Human cDN
	28	15	93.8	819	3	AAC79832	Aac79832 Human sec
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	30	15	93.8	882	6	ABL90324	Abl90324 Human pol
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c	35	15	93.8	1957	10	ADE59228	Ade59228 Human gen
c	36	15	93.8	1957	10	ADE59225	Ade59225 Human gen
	37	15	93.8	2000	11	ACL37128	Acl37128 Rice stre
	38	15	93.8	2004	10	ADB63068	Adb63068 Human cDN
	39	15	93.8	3111	12	ADN38521	Adn38521 Novel hum
	40	15	93.8	3444	11	ADL22622	Adl22622 Human dis
	41	15	93.8	3600	8	ADA83759	Ada83759 Human KIA
	42	15	93.8	3600	12	ADI24494	Adi24494 Human mod
	43	15	93.8	3600	14	ADX83158	Adx83158 Human TEG
	44	15	93.8	3600	14	ADX44432	Adx44432 Human col
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ALIGNMENTS

RESULT 1
AEB28963
ID AEB28963 standard; DNA; 16 BP.
XX
AC AEB28963;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene probe DEL SEQ ID NO:7.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 3; SEQ ID NO 7; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a probe for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 16 BP; 5 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGACCCAGGCCCACAT 16
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Db 1 AGACCCAGGCCCACAT 16

RESULT 2
AAI61022/c
ID AAI61022 standard; cDNA; 1619 BP.
XX
AC AAI61022;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 5011.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM41866.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1; SEQ ID NO 5011; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1619 BP; 350 A; 450 C; 518 G; 301 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 4; Length 1619;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGACCCAGGCCCACAT 16
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Db 1122 AGACCCAGGCCCACAT 1107

RESULT 3
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ID AAI71700 standard; cDNA; 1740 BP.
XX
AC AAI71700;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #2.
XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1740
FT /*tag= a
FT /product= "TLCC-2"
FT /partial
XX
PN WO200177331-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011442.
XX
PR 07-APR-2000; 2000US-00544797.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-010913/01.
DR P-PSDB; AAM51858.
XX
PT Novel isolated human transient receptor potential-like calcium channel
PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
PT pain disorder, and cancer.
XX
PS Claim 1; Fig 1; 148pp; English.
XX
CC The present invention relates to the protein and coding sequences of

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 386.432 Seconds
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Title: US-10-754-446-7
Perfect score: 16
Sequence: 1 agacccaggcccacat 16

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	16	100.0	1400	10	US-11-060-756-7122	Sequence 7122, Ap
4	16	100.0	1740	3	US-09-828-466-3	Sequence 3, Appli
5	16	100.0	1740	5	US-10-103-458-3	Sequence 3, Appli
6	16	100.0	1743	8	US-10-782-695-6	Sequence 6, Appli
7	16	100.0	2051	3	US-09-851-494B-2	Sequence 2, Appli
8	16	100.0	2052	3	US-09-965-529-50	Sequence 50, Appl
9	16	100.0	2052	3	US-09-969-680A-50	Sequence 50, Appl
10	16	100.0	2052	10	US-11-048-692-50	Sequence 50, Appl
11	16	100.0	2092	6	US-10-264-237-920	Sequence 920, App
12	16	100.0	2092	9	US-10-450-763-8078	Sequence 8078, Ap
13	16	100.0	2094	3	US-09-820-893-26	Sequence 26, Appl
14	16	100.0	2094	7	US-10-607-565-26	Sequence 26, Appl
15	16	100.0	2095	3	US-09-828-466-1	Sequence 1, Appli
16	16	100.0	2095	5	US-10-103-458-1	Sequence 1, Appli
17	16	100.0	2095	8	US-10-782-695-4	Sequence 4, Appli
18	16	100.0	2140	8	US-10-723-860-7745	Sequence 7745, Ap
19	16	100.0	13270	3	US-09-851-494B-1	Sequence 1, Appli
20	16	100.0	340449	3	US-09-903-582-3	Sequence 3, Appli
21	15	93.8	342	7	US-10-437-963-97094	Sequence 97094, A
c 22	15	93.8	449	5	US-10-066-543-3155	Sequence 3155, Ap
c 23	15	93.8	552	7	US-10-767-701-22677	Sequence 22677, A
24	15	93.8	558	4	US-09-925-065A-531750	Sequence 531750,
c 25	15	93.8	596	5	US-10-027-632-220987	Sequence 220987,
c 26	15	93.8	596	6	US-10-027-632-220987	Sequence 220987,
c 27	15	93.8	609	4	US-09-925-065A-502281	Sequence 502281,
c 28	15	93.8	614	4	US-09-925-065A-73411	Sequence 73411, A
c 29	15	93.8	614	4	US-09-925-065A-73412	Sequence 73412, A
c 30	15	93.8	614	4	US-09-925-065A-73413	Sequence 73413, A
31	15	93.8	627	4	US-09-925-065A-647660	Sequence 647660,
c 32	15	93.8	675	4	US-09-925-065A-703658	Sequence 703658,
c 33	15	93.8	675	4	US-09-925-065A-703659	Sequence 703659,
c 34	15	93.8	675	4	US-09-925-065A-703660	Sequence 703660,
35	15	93.8	678	8	US-10-425-115-77806	Sequence 77806, A
36	15	93.8	882	5	US-10-106-698-1400	Sequence 1400, Ap
37	15	93.8	882	6	US-10-264-237-886	Sequence 886, App
38	15	93.8	1422	9	US-10-450-763-18881	Sequence 18881, A
39	15	93.8	2004	6	US-10-104-047-1222	Sequence 1222, Ap
40	15	93.8	3600	5	US-10-157-031-41	Sequence 41, Appl
41	15	93.8	3600	8	US-10-651-237-52	Sequence 52, Appl
42	15	93.8	3600	8	US-10-782-413-52	Sequence 52, Appl
c 43	15	93.8	52510	5	US-10-087-192-1006	Sequence 1006, Ap
c 44	15	93.8	59747	7	US-10-450-826-116	Sequence 116, App
c 45	15	93.8	197775	5	US-10-087-192-853	Sequence 853, App

ALIGNMENTS

RESULT 1
US-10-754-446-7
; Sequence 7, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-754-446-7

Query Match 100.0%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-11-060-756-2850
; Sequence 2850, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2850

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;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-2850

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RESULT 3
US-11-060-756-7122
; Sequence 7122, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7122
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-7122

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Db        301 AGACCCAGGCCCACAT 316


RESULT 4
US-09-828-466-3
; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Immaculada
;  TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
;  FILE REFERENCE: MNI-125CP
;  CURRENT APPLICATION NUMBER: US/09/828,466
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 09/544,797
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1740
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1740)
US-09-828-466-3

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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACAT 16
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Db        827 AGACCCAGGCCCACAT 842


RESULT 5
US-10-103-458-3
; Sequence 3, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
;  FILE REFERENCE: MNI-125
;  CURRENT APPLICATION NUMBER: US/10/103,458
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: US/09/544,797
;  PRIOR FILING DATE: PEIOE FILING DATE:  2000-04-07
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1740
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1740)
US-10-103-458-3

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Qy          1 AGACCCAGGCCCACAT 16
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Db        827 AGACCCAGGCCCACAT 842


RESULT 6
US-10-782-695-6
; Sequence 6, Application US/10782695
; Publication No. US20040248160A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Tsai,  Fong-Ying
;  APPLICANT:  Hodge, Martin R.
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Bandaru, Rajasekhar
;  TITLE OF INVENTION: NOVEL 14275, 54420, 8797, 27439, 68730,
;  TITLE OF INVENTION:  69112 AND 52908 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI04-002OMNIM
;  CURRENT APPLICATION NUMBER: US/10/782,695
;  CURRENT FILING DATE:  2004-02-19
;  PRIOR APPLICATION NUMBER: US 09/945,254
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/229,829
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: US 09/945,301
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/229,301
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: US 10/007,399
;  PRIOR FILING DATE: 2001-11-05
;  PRIOR APPLICATION NUMBER: US 09/390,039
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: US 09/146,416
;  PRIOR FILING DATE: 1998-09-03
;  PRIOR APPLICATION NUMBER: US 10/024,036
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US 60/258,222
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 10/103,458
;  PRIOR FILING DATE: 2002-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	172147	7	US-11-112-908-22	Sequence 22, Appl
	2	16	100.0	188682	7	US-11-112-908-23	Sequence 23, Appl
	3	15	93.8	22	6	US-10-310-914A-1360219	Sequence 1360219,
	4	15	93.8	25	6	US-10-310-914A-1360184	Sequence 1360184,
	5	15	93.8	403278	6	US-10-995-561-13421	Sequence 13421, A
	6	14.4	90.0	19	8	US-11-101-244-97619	Sequence 97619, A
	7	14.4	90.0	19	8	US-11-101-244-97633	Sequence 97633, A
	8	14.4	90.0	19	9	US-11-083-784-97619	Sequence 97619, A
	9	14.4	90.0	19	9	US-11-083-784-97633	Sequence 97633, A
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	11	14.4	90.0	791	6	US-10-750-623-62019	Sequence 62019, A
	12	14.4	90.0	1214	7	US-11-112-908-134	Sequence 134, App
c	13	14.4	90.0	1889	6	US-10-821-234-37	Sequence 37, Appl
	14	14.4	90.0	2215	7	US-11-112-908-144	Sequence 144, App
	15	14.4	90.0	2453	6	US-10-750-185-36539	Sequence 36539, A
	16	14.4	90.0	2453	6	US-10-750-623-36539	Sequence 36539, A
	17	14.4	90.0	44848	7	US-11-106-672A-42	Sequence 42, Appl
c	18	14.4	90.0	54767	6	US-10-995-561-13357	Sequence 13357, A
	19	14.4	90.0	158410	7	US-11-121-086-46	Sequence 46, Appl
c	20	14.4	90.0	164810	7	US-11-121-086-4	Sequence 4, Appli
	21	14.4	90.0	180862	7	US-11-112-908-40	Sequence 40, Appl
	22	14.4	90.0	189539	7	US-11-121-086-16	Sequence 16, Appl
	23	14	87.5	201	7	US-11-124-368A-4143	Sequence 4143, Ap
	24	14	87.5	496	6	US-10-750-185-37291	Sequence 37291, A
	25	14	87.5	496	6	US-10-750-623-37291	Sequence 37291, A
	26	14	87.5	600	7	US-11-136-527-6328	Sequence 6328, Ap
c	27	14	87.5	1038	6	US-10-512-109-16	Sequence 16, Appl
c	28	14	87.5	1223	6	US-10-512-109-3	Sequence 3, Appli
c	29	14	87.5	1223	6	US-10-512-109-14	Sequence 14, Appl
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	31	14	87.5	1816	6	US-10-750-623-29826	Sequence 29826, A
c	32	14	87.5	2378	6	US-10-821-234-117	Sequence 117, App
	33	14	87.5	3884	6	US-10-131-826A-145	Sequence 145, App
	34	14	87.5	10705	7	US-11-136-527-2232	Sequence 2232, Ap
	35	14	87.5	20945	6	US-10-995-561-13463	Sequence 13463, A
	36	14	87.5	23082	6	US-10-995-561-13457	Sequence 13457, A
	37	14	87.5	27615	7	US-11-136-527-514	Sequence 514, App
c	38	14	87.5	94510	6	US-10-995-561-13332	Sequence 13332, A
c	39	14	87.5	103660	6	US-10-995-561-13253	Sequence 13253, A
	40	14	87.5	197096	7	US-11-121-086-107	Sequence 107, App
	41	13.4	83.8	19	6	US-10-310-914A-1165996	Sequence 1165996,
	42	13.4	83.8	19	8	US-11-101-244-798463	Sequence 798463,
	43	13.4	83.8	19	9	US-11-083-784-798463	Sequence 798463,
	44	13.4	83.8	21	6	US-10-310-914A-1130386	Sequence 1130386,
	45	13.4	83.8	23	6	US-10-310-914A-223914	Sequence 223914,

ALIGNMENTS

RESULT 1
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

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Best Local Similarity 100.0%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 23, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908

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;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 188682
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-23

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Db      66280 AGACCCAGGCCCACAT 66295


RESULT 3
US-10-310-914A-1360219
; Sequence 1360219, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1360219
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1360219

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACA 15
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Db          8 AGACCCAGGCCCACA 22


RESULT 4
US-10-310-914A-1360184
; Sequence 1360184, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1360184
;   LENGTH: 25
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1360184

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACA 15
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Db          2 AGACCCAGGCCCACA 16


RESULT 5
US-10-995-561-13421
; Sequence 13421, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13421
;   LENGTH: 403278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(403278)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2
US-10-995-561-13421

  Query Match             93.8%;  Score 15;  DB 6;  Length 403278;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACA 15
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Db     197280 AGACCCAGGCCCACA 197294


RESULT 6
US-11-101-244-97619
; Sequence 97619, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 97619
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-97619

  Query Match             90.0%;  Score 14.4;  DB 8;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:32:47 ; Search time 58.24 Seconds
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Perfect score: 16
Sequence: 1 agacccaggcccacat 16

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		16	100.0	601	3	US-09-949-016-59085	Sequence 59085, A
2		16	100.0	2051	3	US-09-949-016-1712	Sequence 1712, Ap
3		16	100.0	15353	3	US-09-949-016-13454	Sequence 13454, A
4		15	93.8	2004	3	US-10-104-047-1222	Sequence 1222, Ap
5	c	15	93.8	56963	3	US-09-949-016-12966	Sequence 12966, A
6	c	15	93.8	56968	3	US-09-949-016-11888	Sequence 11888, A
7		15	93.8	254366	3	US-09-822-871-3	Sequence 3, Appli
8		14.4	90.0	256	3	US-09-513-999C-25589	Sequence 25589, A
9	c	14.4	90.0	533	3	US-09-270-767-9339	Sequence 9339, Ap
10	c	14.4	90.0	533	3	US-09-270-767-24621	Sequence 24621, A
11	c	14.4	90.0	601	3	US-09-949-016-31585	Sequence 31585, A
12	c	14.4	90.0	601	3	US-09-949-016-31586	Sequence 31586, A
13		14.4	90.0	601	3	US-09-949-016-91141	Sequence 91141, A
14	c	14.4	90.0	601	3	US-09-949-016-94698	Sequence 94698, A
15	c	14.4	90.0	601	3	US-09-949-016-94699	Sequence 94699, A
16	c	14.4	90.0	601	3	US-09-949-016-151080	Sequence 151080,
17	c	14.4	90.0	601	3	US-09-949-016-151081	Sequence 151081,
18		14.4	90.0	1224	3	US-09-581-105-7	Sequence 7, Appli
19		14.4	90.0	2502	2	US-08-073-384C-7	Sequence 7, Appli
20		14.4	90.0	2502	2	US-08-254-359A-7	Sequence 7, Appli
21		14.4	90.0	2502	2	US-08-483-043-7	Sequence 7, Appli
22		14.4	90.0	2502	2	US-08-481-238-7	Sequence 7, Appli
23		14.4	90.0	2502	2	US-08-471-066B-7	Sequence 7, Appli
24		14.4	90.0	2502	2	US-08-484-956-7	Sequence 7, Appli
25		14.4	90.0	2502	2	US-08-757-653-7	Sequence 7, Appli
26		14.4	90.0	2502	2	US-08-599-491-7	Sequence 7, Appli
27		14.4	90.0	2502	2	US-08-756-386-7	Sequence 7, Appli
28		14.4	90.0	2502	2	US-08-823-516-7	Sequence 7, Appli
29		14.4	90.0	2502	3	US-08-682-853A-7	Sequence 7, Appli
30		14.4	90.0	2502	3	US-08-759-038-7	Sequence 7, Appli
31		14.4	90.0	2502	3	US-08-758-314-7	Sequence 7, Appli
32		14.4	90.0	2502	3	US-09-350-309-7	Sequence 7, Appli
33		14.4	90.0	2502	3	US-08-520-946-7	Sequence 7, Appli
34		14.4	90.0	2502	3	US-09-684-938-7	Sequence 7, Appli
35		14.4	90.0	2502	3	US-09-308-825A-7	Sequence 7, Appli
36		14.4	90.0	2502	3	US-09-758-282B-7	Sequence 7, Appli
37		14.4	90.0	2502	3	US-09-655-378A-7	Sequence 7, Appli
38		14.4	90.0	2502	3	US-09-940-244-7	Sequence 7, Appli
39		14.4	90.0	2502	3	US-09-333-145-7	Sequence 7, Appli
40		14.4	90.0	2502	3	US-09-577-304A-7	Sequence 7, Appli
41		14.4	90.0	2502	3	US-09-381-212-7	Sequence 7, Appli
42		14.4	90.0	2502	3	US-10-081-806-7	Sequence 7, Appli
43		14.4	90.0	2502	3	US-09-713-601A-7	Sequence 7, Appli
44		14.4	90.0	2601	3	US-10-104-047-1515	Sequence 1515, Ap
45		14.4	90.0	3496	3	US-08-660-451A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-59085
; Sequence 59085, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59085
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59085

Query Match 100.0%; Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        449 AGACCCAGGCCCACAT 464
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RESULT 2
US-09-949-016-1712
; Sequence 1712, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1712
;   LENGTH: 2051
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1712

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  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACAT 16
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Db        952 AGACCCAGGCCCACAT 967


RESULT 3
US-09-949-016-13454
; Sequence 13454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13454
;   LENGTH: 15353
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13454

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Qy          1 AGACCCAGGCCCACAT 16
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Db       7582 AGACCCAGGCCCACAT 7597


RESULT 4
US-10-104-047-1222
; Sequence 1222, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1222
;   LENGTH: 2004
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-104-047-1222

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  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
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Db       1721 GACCCAGGCCCACAT 1735


RESULT 5
US-09-949-016-12966/c
; Sequence 12966, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12966
;   LENGTH: 56963
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12966

  Query Match             93.8%;  Score 15;  DB 3;  Length 56963;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGACCCAGGCCCACA 15
              |||||||||||||||
Db      45193 AGACCCAGGCCCACA 45179


RESULT 6
US-09-949-016-11888/c
; Sequence 11888, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11888
;   LENGTH: 56968
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11888

  Query Match             93.8%;  Score 15;  DB 3;  Length 56968;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:49:05 ; Search time 785.792 Seconds
(without alignments)
1157.425 Million cell updates/sec

Title: US-10-754-446-5
Perfect score: 16
Sequence: 1 tctgcccacagtacct 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		16	100.0	790	8	AF305572S3	AF305574 Homo sapi
2	c	16	100.0	2551	5	AJ720988	AJ720988 Gallus ga
3		16	100.0	7939	4	AF292105	AF292105 Sus scrof
4		16	100.0	13270	8	AF287270	AF287270 Homo sapi
5	c	16	100.0	46941	8	AL583835	AL583835 Human DNA
6		16	100.0	104062	5	CR855371	CR855371 Chicken D
7	c	16	100.0	138616	14	AC115525	AC115525 Rattus no
8	c	16	100.0	155645	14	AC021153	AC021153 Homo sapi
9	c	16	100.0	166504	8	AC008275	AC008275 Homo sapi
10		16	100.0	173126	8	AC008878	AC008878 Homo sapi
11	c	16	100.0	188149	14	AC151428	AC151428 Otolemur
12		16	100.0	190284	14	AC115524	AC115524 Rattus no
13		16	100.0	215397	8	AL355497	AL355497 Human DNA
14	c	16	100.0	215470	14	AC147936	AC147936 Otolemur
15		16	100.0	226981	14	AC127822	AC127822 Rattus no
16	c	16	100.0	256594	14	AC133700	AC133700 Rattus no
17	c	15	93.8	310	6	CQ687156	CQ687156 Sequence
18		15	93.8	523	10	BV427581	BV427581 S237P6504
19	c	15	93.8	622	10	BV315511	BV315511 S236P6394
20	c	15	93.8	670	10	BV025162	BV025162 S212P6124
21	c	15	93.8	1525	5	CR386310	CR386310 Gallus ga
22	c	15	93.8	4992	5	AJ720888	AJ720888 Gallus ga
23		15	93.8	5210	9	AK122332	AK122332 Mus muscu
24		15	93.8	6331	13	EMVRPVP	J04374 Eggplant mo
25	c	15	93.8	62000	8	AP001984	AP001984 Homo sapi
26	c	15	93.8	110000	1	CP000082_24	Continuation (25 o
27	c	15	93.8	110000	14	AC118875_2	Continuation (3 of
28	c	15	93.8	118103	14	AC009817	AC009817 Homo sapi
29	c	15	93.8	134697	8	AC114738	AC114738 Homo sapi
30	c	15	93.8	138317	8	AP003481	AP003481 Homo sapi
31		15	93.8	139512	8	HSJ1169J3	AL049652 Human DNA
32	c	15	93.8	140968	9	BX537299	BX537299 Mouse DNA
33		15	93.8	151698	14	AC132644	AC132644 Rattus no
34	c	15	93.8	152816	14	AC079739	AC079739 Homo sapi
35		15	93.8	156808	14	AC012407	AC012407 Homo sapi
36		15	93.8	161100	14	AC025659	AC025659 Homo sapi
37	c	15	93.8	161179	14	AC083954	AC083954 Homo sapi
38		15	93.8	161362	14	AL355503	AL355503 Homo sapi
39	c	15	93.8	167322	14	AC016788	AC016788 Homo sapi
40	c	15	93.8	168789	9	AC127318	AC127318 Mus muscu
41	c	15	93.8	171141	9	AC157651	AC157651 Mus muscu
42	c	15	93.8	172160	9	AC119996	AC119996 Mus muscu
43	c	15	93.8	172772	9	AC121923	AC121923 Mus muscu
44		15	93.8	173805	9	AC124548	AC124548 Mus muscu
45	c	15	93.8	175048	14	AC161042	AC161042 Mus muscu

ALIGNMENTS

RESULT 1
AF305572S3
LOCUS AF305572S3 790 bp DNA linear PRI 26-DEC-2000
DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 3 and 4.
ACCESSION AF305574
VERSION AF305574.1 GI:11991200
KEYWORDS .
SEGMENT 3 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
PUBMED 10973263
REFERENCE 2 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES Location/Qualifiers
source 1. .790
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
exon 267. .434
/gene="MCOLN1"
/number=3
exon 589. .757
/gene="MCOLN1"
/number=4
ORIGIN

Query Match 100.0%; Score 16; DB 8; Length 790;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db        578 TCTGCCCACAGTACCT 593


RESULT 2
AJ720988/c
LOCUS       AJ720988               2551 bp    mRNA    linear   VRT 12-JAN-2005
DEFINITION  Gallus gallus mRNA for hypothetical protein, clone 31p4.
ACCESSION   AJ720988
VERSION     AJ720988.1  GI:53136635
KEYWORDS    ORF1.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1
  AUTHORS   Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J.,
            Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M.,
            Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
  TITLE     Full-length cDNAs from chicken bursal lymphocytes to facilitate
            gene function analysis
  JOURNAL   Genome Biol. 6 (1), R6 (2005)
   PUBMED   15642098
REFERENCE   2  (bases 1 to 2551)
  AUTHORS   Caldwell,R.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum,
            Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
            1, D-85764 Neuherberg, GERMANY
FEATURES             Location/Qualifiers
     source          1. .2551
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="CB"
                     /db_xref="taxon:9031"
                     /clone="31p4"
                     /cell_type="lymphocyte"
                     /tissue_type="bursa"
                     /clone_lib="riken1"
                     /dev_stage="2 weeks old"
     gene            1. .2551
                     /locus_tag="RCJMB04_31p4"
     5'UTR           <1. .50
                     /locus_tag="RCJMB04_31p4"
     CDS             51. .608
                     /locus_tag="RCJMB04_31p4"
                     /note="ORF1"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="CAG32647.1"
                     /db_xref="GI:53136636"
                     /db_xref="UniProt/TrEMBL:Q5ZHZ6"
                     /translation="MRLIFSGAVCALQALTLLLLLGPLGNAFAEVNITNTSYNVTSSP
                     VVQGNNSASNSSAVPSTQSAAGTPTSASHPTSASHATNASHPSSTTAHVTVPSQPAET
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                     LCVLVILYIGCKTYHSEKRHSVQNH"
     3'UTR           609. .>2551
                     /locus_tag="RCJMB04_31p4"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 5;  Length 2551;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db       1325 TCTGCCCACAGTACCT 1310


RESULT 3
```

```
AF292105
LOCUS       AF292105               7939 bp    DNA     linear   MAM 24-APR-2001
DEFINITION  Sus scrofa uteroferrin (ACP5) gene, complete cds.
ACCESSION   AF292105
VERSION     AF292105.1  GI:9965376
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 7939)
  AUTHORS   Vallet,J.L. and Fahrenkrug,S.C.
  TITLE     Structure of the gene for uteroferrin
  JOURNAL   DNA Cell Biol. 19 (11), 689-696 (2000)
   PUBMED   11098218
REFERENCE   2  (bases 1 to 7939)
  AUTHORS   Vallet,J.L. and Fahrenkrug,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2000) Reproduction Research Unit, U.S. Meat
            Animal Research Center, P.O. Box 166, Clay Center, NE 68933, USA
FEATURES             Location/Qualifiers
     source          1. .7939
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
     gene            3229. .5516
                     /gene="ACP5"
     mRNA            join(3229. .3320,3463. .3747,3952. .4079,4219. .4564,
                     4923. .5516)
                     /gene="ACP5"
                     /product="utoferrin"
     exon            3229. .3320
                     /gene="ACP5"
                     /number=1
     CDS             join(3463. .3747,3952. .4079,4219. .4564,4923. .5186)
                     /gene="ACP5"
                     /function="iron transporter"
                     /note="tartrate resistant acid phosphatase"
                     /codon_start=1
                     /product="uteroferrin"
                     /protein_id="AAG10065.1"
                     /db_xref="GI:9965377"
                     /translation="MDTWTVLLILQASLVLPGAVGTRTNTRTAPTPILRFVAVGDWGG
                     VPNAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDAKDKRFQETFEDVF
                     SDPSLRNVPWHVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYYRLRFKIPRSNVSVAI
                     FMLDTVTLCGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYPVWS
                     IAEHGPTHCLVKQLLPLLTTHKVTAYLCGHDHNLQYLQDENGLGFVLSGAGNFMDPSK
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                     HQHRRA"
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                     /gene="ACP5"
                     /number=2
     exon            3952. .4079
                     /gene="ACP5"
                     /number=3
     exon            4219. .4564
                     /gene="ACP5"
                     /number=4
     exon            4923. .5516
                     /gene="ACP5"
                     /number=5
ORIGIN

  Query Match             100.0%;  Score 16;  DB 4;  Length 7939;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db       4912 TCTGCCCACAGTACCT 4927
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 1789.31 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-5
Perfect score: 16
Sequence: 1 tctgcccacagtacct 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16	100.0	154	9	BH271054	BH271054 CH230-162
	2	16	100.0	480	2	BB856429	BB856429 BB856429
	3	16	100.0	525	9	AQ669413	AQ669413 HS_5407_B
c	4	16	100.0	696	1	AJ727930	AJ727930 AJ727930
	5	16	100.0	745	1	AJ727936	AJ727936 AJ727936
	6	16	100.0	762	5	BU306972	BU306972 603612510
	7	16	100.0	774	8	DR431852	DR431852 nax48f12.
	8	16	100.0	806	5	BU383135	BU383135 603861896
	9	16	100.0	1008	5	BU420692	BU420692 603231561
c	10	15	93.8	224	8	CV972084	CV972084 LRRGE0208
c	11	15	93.8	269	8	CV972398	CV972398 LRRGE0239
	12	15	93.8	279	1	BB007743	BB007743 BB007743
	13	15	93.8	279	8	CV972703	CV972703 LRRGE0270
	14	15	93.8	281	8	CV888115	CV888115 LRRGE0000
c	15	15	93.8	361	8	CV972086	CV972086 LRRGE0208
	16	15	93.8	388	5	BY619013	BY619013 BY619013
c	17	15	93.8	420	9	BH273644	BH273644 CH230-70E
c	18	15	93.8	436	8	CV888113	CV888113 LRRGE0000
	19	15	93.8	475	8	CV888114	CV888114 LRRGE0000
c	20	15	93.8	492	9	AZ822326	AZ822326 2M0095J01
c	21	15	93.8	501	9	BH117609	BH117609 RPCI-24-2
	22	15	93.8	507	9	AZ768935	AZ768935 1M0569J09
	23	15	93.8	517	9	AZ585292	AZ585292 1M0390F20
	24	15	93.8	525	9	AQ357179	AQ357179 CITBI-E1-
c	25	15	93.8	591	10	CE537462	CE537462 tigr-gss-
	26	15	93.8	595	2	BG404774	BG404774 602420961
c	27	15	93.8	599	1	AI412276	AI412276 EST240572
	28	15	93.8	625	7	CK620962	CK620962 ml18e10.y
	29	15	93.8	672	10	CE809412	CE809412 tigr-gss-
	30	15	93.8	714	5	BY764892	BY764892 BY764892
	31	15	93.8	727	1	AJ724937	AJ724937 AJ724937
c	32	15	93.8	727	5	BU139411	BU139411 603134255
c	33	15	93.8	732	1	AJ724931	AJ724931 AJ724931
c	34	15	93.8	734	10	CE812263	CE812263 tigr-gss-
	35	15	93.8	745	11	CR081738	CR081738 Forward s
c	36	15	93.8	753	10	AG457089	AG457089 Mus muscu
	37	15	93.8	763	11	CR228261	CR228261 Reverse s
c	38	15	93.8	784	3	BI331708	BI331708 602982759
	39	15	93.8	784	7	CF924020	CF924020 DD014B09.
	40	15	93.8	790	7	CN234992	CN234992 WLA104G03
c	41	15	93.8	797	7	CK315394	CK315394 SB02024B2
	42	15	93.8	870	11	CR118310	CR118310 Reverse s
c	43	15	93.8	999	2	BF976532	BF976532 602244386
c	44	15	93.8	1001	5	BU192451	BU192451 AGENCOURT
	45	15	93.8	1184	7	CK167560	CK167560 FGAS05194

ALIGNMENTS

RESULT 1
BH271054/c
LOCUS BH271054 154 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-162L17.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-162L17, genomic survey sequence.
ACCESSION BH271054
VERSION BH271054.1 GI:17183456
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 154)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-162L17.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 162 row: L column: 17
Seq primer: SP6
Class: BAC ends.
FEATURES Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-162L17"
/sex="Female"
/cell_type="Brain"

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                     /clone_lib="CHORI-230 Segment 1"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 9;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db        150 TCTGCCCACAGTACCT 135


RESULT 2
BB856429
LOCUS       BB856429                 480 bp    mRNA    linear   EST 26-NOV-2001
DEFINITION  BB856429 RIKEN full-length enriched, B16 F10Y cells Mus musculus
            cDNA clone G370034I10 5', mRNA sequence.
ACCESSION   BB856429
VERSION     BB856429.1  GI:17097883
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
            Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
            Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
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Qy          1 TCTGCCCACAGTACCT 16
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Db        366 TCTGCCCACAGTACCT 381


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VERSION     AQ669413.1  GI:5202159
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 983  row: L  column: 19
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            High quality sequence stop: 525.
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                     /sex="male"
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ORIGIN

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 217.088 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-5
Perfect score: 16
Sequence: 1 tctgcccacagtacct 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	16	100.0	20046	4	AAK73826	Aak73826 Human imm
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	7	15	93.8	177531	10	ADB87936	Adb87936 Human UGT
	8	15	93.8	177531	10	ADB96919	Adb96919 Human MDR
	9	15	93.8	177531	10	ADB92110	Adb92110 Human MDR
	10	15	93.8	177531	10	ADH74617	Adh74617 Human BAC
	11	14.4	90.0	405	4	AAL35222	Aal35222 Human mus
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	28	14.4	90.0	2317	6	ABS76414	Abs76414 cDNA enco
	29	14.4	90.0	2317	6	ABV99386	Abv99386 Human NOV
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	37	14.4	90.0	2452	6	AAI71445	Aai71445 TNFR/NGER
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c	45	14.4	90.0	4376	10	ADF50290	Adf50290 Human PFM

ALIGNMENTS

RESULT 1
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XX
AC AEB28961;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene probe IVS WT SEQ ID NO:5.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 3; SEQ ID NO 5; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a probe for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 16 BP; 3 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCTGCCCACAGTACCT 16

RESULT 2
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AC AAK73827;
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DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.
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KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
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PF 17-JAN-2001; 2001WO-US001354.
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PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 08-NOV-2000; 2000US-0246610P.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 386.432 Seconds
(without alignments)
342.389 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	16	100.0	653	4	US-09-925-065A-696499	Sequence 696499,
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	18	14.4	90.0	297	3	US-09-783-590-8724	Sequence 8724, Ap
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	20	14.4	90.0	388	3	US-09-783-590-8696	Sequence 8696, Ap
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	27	14.4	90.0	452	4	US-09-925-065A-256794	Sequence 256794,
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c	34	14.4	90.0	585	5	US-10-027-632-229737	Sequence 229737,
c	35	14.4	90.0	585	5	US-10-027-632-229738	Sequence 229738,
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	39	14.4	90.0	606	4	US-09-925-065A-495309	Sequence 495309,
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	41	14.4	90.0	626	4	US-09-925-065A-539208	Sequence 539208,
	42	14.4	90.0	626	4	US-09-925-065A-539209	Sequence 539209,
	43	14.4	90.0	630	5	US-10-027-632-275537	Sequence 275537,
	44	14.4	90.0	630	6	US-10-027-632-275537	Sequence 275537,
c	45	14.4	90.0	655	4	US-09-925-065A-397489	Sequence 397489,

ALIGNMENTS

RESULT 1
US-10-754-446-5
; Sequence 5, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-754-446-5

Query Match 100.0%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGCCCACAGTACCT 16
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Db 1 TCTGCCCACAGTACCT 16

RESULT 2
US-09-925-065A-696499
; Sequence 696499, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

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;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 696499
;   LENGTH: 653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-696499

  Query Match           100.0%;  Score 16;  DB 4;  Length 653;
  Best Local Similarity  100.0%;  Pred. No. 73;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db        137 TCTGCCCACAGTACCT 152


RESULT 3
US-09-925-065A-696500
; Sequence 696500, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 696500
;   LENGTH: 653
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-696500

  Query Match           100.0%;  Score 16;  DB 4;  Length 653;
  Best Local Similarity  100.0%;  Pred. No. 73;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
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Db        137 TCTGCCCACAGTACCT 152


RESULT 4
US-09-851-494B-1
; Sequence 1, Application US/09851494B
; Publication No. US20030064363A1
; GENERAL INFORMATION:
;  APPLICANT: ML4 Foundation
;  APPLICANT:  Goldin, Ehud
;  APPLICANT:  Slaugenhaupt, Susan A.
;  APPLICANT:  Sun, Mei
;  APPLICANT:  Acierno, James S.
;  TITLE OF INVENTION: A Gene Encoding A New TRP Channel is Mutated in Mucolipidosis IV
;  FILE REFERENCE: 3394/1H557US1
;  CURRENT APPLICATION NUMBER: US/09/851,494B
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 13270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-494B-1

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Qy          1 TCTGCCCACAGTACCT 16
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Db       5525 TCTGCCCACAGTACCT 5540


RESULT 5
US-10-972-079-69742
; Sequence 69742, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  KERR, Richard
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  HOLM, Tom
;  TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
;  TITLE OF INVENTION:  LIVESTOCK
;  FILE REFERENCE: MMI1110-2
;  CURRENT APPLICATION NUMBER: US/10/972,079
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,333
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 96631
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 69742
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Chicken  19866894342124_1
US-10-972-079-69742

  Query Match           97.5%;  Score 15.6;  DB 9;  Length 600;
  Best Local Similarity  93.8%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              :|||||||||||||||
Db        461 WCTGCCCACAGTACCT 476


RESULT 6
US-10-972-079-69743
; Sequence 69743, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  KERR, Richard
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  HOLM, Tom
;  TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
;  TITLE OF INVENTION:  LIVESTOCK
;  FILE REFERENCE: MMI1110-2
;  CURRENT APPLICATION NUMBER: US/10/972,079
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,333
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 96631
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
65.779 Million cell updates/sec

Title: US-10-754-446-5
Perfect score: 16
Sequence: 1 tctgcccacagtacct 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.4	90.0	69	6	US-10-310-914A-10301	Sequence 10301, A
	2	14.4	90.0	69	6	US-10-310-914A-16743	Sequence 16743, A
c	3	14.4	90.0	1126	6	US-10-750-185-61765	Sequence 61765, A
c	4	14.4	90.0	1126	6	US-10-750-623-61765	Sequence 61765, A
c	5	14.4	90.0	2095	6	US-10-750-185-48943	Sequence 48943, A
c	6	14.4	90.0	2095	6	US-10-750-623-48943	Sequence 48943, A
	7	14.4	90.0	3396	6	US-10-750-185-57338	Sequence 57338, A
	8	14.4	90.0	3396	6	US-10-750-623-57338	Sequence 57338, A
c	9	14.4	90.0	40644	6	US-10-995-561-13480	Sequence 13480, A
	10	14.4	90.0	340000	7	US-11-102-978-3	Sequence 3, Appli
	11	14	87.5	201	6	US-10-995-561-18449	Sequence 18449, A
c	12	14	87.5	201	6	US-10-995-561-24263	Sequence 24263, A
c	13	14	87.5	201	6	US-10-995-561-24481	Sequence 24481, A
	14	14	87.5	600	7	US-11-136-527-5051	Sequence 5051, Ap
c	15	14	87.5	624	7	US-11-136-527-955	Sequence 955, App
c	16	14	87.5	625	6	US-10-750-185-54379	Sequence 54379, A
c	17	14	87.5	625	6	US-10-750-623-54379	Sequence 54379, A
c	18	14	87.5	159138	6	US-10-995-561-13230	Sequence 13230, A
	19	14	87.5	241805	6	US-10-995-561-13215	Sequence 13215, A
c	20	13.4	83.8	25	7	US-11-121-849-620404	Sequence 620404,
c	21	13.4	83.8	25	7	US-11-121-849-638454	Sequence 638454,
	22	13.4	83.8	201	6	US-10-995-561-18604	Sequence 18604, A
c	23	13.4	83.8	447	7	US-11-136-527-3908	Sequence 3908, Ap
	24	13.4	83.8	447	7	US-11-136-527-8004	Sequence 8004, Ap
c	25	13.4	83.8	526	7	US-11-128-061-2758	Sequence 2758, Ap
c	26	13.4	83.8	526	7	US-11-128-061-6400	Sequence 6400, Ap
c	27	13.4	83.8	590	6	US-10-750-185-38148	Sequence 38148, A
c	28	13.4	83.8	590	6	US-10-750-623-38148	Sequence 38148, A
c	29	13.4	83.8	600	6	US-10-750-185-577	Sequence 577, App
c	30	13.4	83.8	600	6	US-10-750-185-3763	Sequence 3763, Ap
c	31	13.4	83.8	600	6	US-10-750-623-577	Sequence 577, App
c	32	13.4	83.8	600	6	US-10-750-623-3763	Sequence 3763, Ap
	33	13.4	83.8	1366	7	US-11-128-061-1067	Sequence 1067, Ap
c	34	13.4	83.8	1414	6	US-10-750-185-43019	Sequence 43019, A
c	35	13.4	83.8	1414	6	US-10-750-623-43019	Sequence 43019, A
c	36	13.4	83.8	1725	6	US-10-750-185-32683	Sequence 32683, A
c	37	13.4	83.8	1725	6	US-10-750-623-32683	Sequence 32683, A
c	38	13.4	83.8	1751	6	US-10-750-185-27624	Sequence 27624, A
c	39	13.4	83.8	1751	6	US-10-750-623-27624	Sequence 27624, A
c	40	13.4	83.8	1833	6	US-10-750-185-38394	Sequence 38394, A
c	41	13.4	83.8	1833	6	US-10-750-623-38394	Sequence 38394, A
c	42	13.4	83.8	1865	6	US-10-750-185-61413	Sequence 61413, A
c	43	13.4	83.8	1865	6	US-10-750-623-61413	Sequence 61413, A
c	44	13.4	83.8	2149	7	US-11-078-189-6	Sequence 6, Appli
c	45	13.4	83.8	2478	6	US-10-750-185-40981	Sequence 40981, A

ALIGNMENTS

RESULT 1
US-10-310-914A-10301
; Sequence 10301, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10301
; LENGTH: 69
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-10301

Query Match 90.0%; Score 14.4; DB 6; Length 69;
Best Local Similarity 68.8%; Pred. No. 73;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TCTGCCCACAGTACCT 16
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Db         28 UCUGCACACAGUACCU 43
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RESULT 2
US-10-310-914A-16743
; Sequence 16743, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16743
; LENGTH: 69
; TYPE: RNA

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;   ORGANISM: Human
US-10-310-914A-16743

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 69;
  Best Local Similarity   68.8%;  Pred. No. 73;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              :|:|| |||||:|||:
Db         28 UCUGCACACAGUACCU 43


RESULT 3
US-10-750-185-61765/c
; Sequence 61765, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61765
;   LENGTH: 1126
;   TYPE: DNA
;   ORGANISM: Bovine  19866881607649
US-10-750-185-61765

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 1126;
  Best Local Similarity   93.8%;  Pred. No. 80;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              |||| ||||||||||||
Db        599 TCTGGCCACAGTACCT 584


RESULT 4
US-10-750-623-61765/c
; Sequence 61765, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61765
;   LENGTH: 1126
;   TYPE: DNA
;   ORGANISM: Bovine  19866881607649
US-10-750-623-61765

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 1126;
  Best Local Similarity   93.8%;  Pred. No. 80;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              |||| ||||||||||||
Db        599 TCTGGCCACAGTACCT 584


RESULT 5
US-10-750-185-48943/c
; Sequence 48943, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48943
;   LENGTH: 2095
;   TYPE: DNA
;   ORGANISM: Bovine  19866881228818
US-10-750-185-48943

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 2095;
  Best Local Similarity   93.8%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
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Db       1253 TCTGCCCACAGCACCT 1238


RESULT 6
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; Sequence 48943, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48943
;   LENGTH: 2095
;   TYPE: DNA
;   ORGANISM: Bovine  19866881228818
US-10-750-623-48943

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 2095;
  Best Local Similarity   93.8%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	14.4	90.0	601	3	US-09-949-016-22226	Sequence 22226, A
	4	14.4	90.0	601	3	US-09-949-016-22227	Sequence 22227, A
	5	14.4	90.0	601	3	US-09-949-016-22228	Sequence 22228, A
	6	14.4	90.0	601	3	US-09-949-016-22229	Sequence 22229, A
	7	14.4	90.0	601	3	US-09-949-016-22230	Sequence 22230, A
	8	14.4	90.0	601	3	US-09-949-016-22231	Sequence 22231, A
	9	14.4	90.0	601	3	US-09-949-016-22232	Sequence 22232, A
	10	14.4	90.0	601	3	US-09-949-016-22233	Sequence 22233, A
c	11	14.4	90.0	601	3	US-09-949-016-38209	Sequence 38209, A
c	12	14.4	90.0	601	3	US-09-949-016-38210	Sequence 38210, A
c	13	14.4	90.0	601	3	US-09-949-016-38211	Sequence 38211, A
	14	14.4	90.0	601	3	US-09-949-016-51333	Sequence 51333, A
	15	14.4	90.0	601	3	US-09-949-016-51334	Sequence 51334, A
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	18	14.4	90.0	601	3	US-09-949-016-51337	Sequence 51337, A
	19	14.4	90.0	601	3	US-09-949-016-51338	Sequence 51338, A
	20	14.4	90.0	601	3	US-09-949-016-51339	Sequence 51339, A
	21	14.4	90.0	601	3	US-09-949-016-51340	Sequence 51340, A
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c	24	14.4	90.0	601	3	US-09-949-016-68415	Sequence 68415, A
c	25	14.4	90.0	601	3	US-09-949-016-169541	Sequence 169541,
c	26	14.4	90.0	601	3	US-09-949-016-169542	Sequence 169542,
c	27	14.4	90.0	601	3	US-09-949-016-169543	Sequence 169543,
c	28	14.4	90.0	789	3	US-08-986-765-4	Sequence 4, Appli
	29	14.4	90.0	2569	3	US-10-104-047-452	Sequence 452, App
	30	14.4	90.0	2883	3	US-09-614-221A-371	Sequence 371, App
	31	14.4	90.0	3025	2	US-08-444-734A-1	Sequence 1, Appli
c	32	14.4	90.0	3778	3	US-09-799-451-160	Sequence 160, App
c	33	14.4	90.0	4376	3	US-10-200-012-15	Sequence 15, Appl
	34	14.4	90.0	4521	3	US-09-533-494A-18	Sequence 18, Appl
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c	36	14.4	90.0	12055	3	US-09-949-016-13233	Sequence 13233, A
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	38	14.4	90.0	71119	3	US-09-949-016-15358	Sequence 15358, A
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c	40	14.4	90.0	77663	3	US-09-949-016-13751	Sequence 13751, A
c	41	14.4	90.0	121427	3	US-09-949-016-11950	Sequence 11950, A
c	42	14.4	90.0	121433	3	US-09-949-016-13230	Sequence 13230, A
c	43	14.4	90.0	160759	3	US-09-949-016-16514	Sequence 16514, A
c	44	14	87.5	601	3	US-09-949-016-117072	Sequence 117072,
c	45	14	87.5	601	3	US-09-949-016-152388	Sequence 152388,

ALIGNMENTS

RESULT 1
US-09-949-016-13454
; Sequence 13454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13454
; LENGTH: 15353
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13454

Query Match 100.0%; Score 16; DB 3; Length 15353;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGCCCACAGTACCT 16
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Db 6125 TCTGCCCACAGTACCT 6140

RESULT 2
US-09-949-016-13427/c
; Sequence 13427, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13427
;   LENGTH: 110585
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(110585)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13427

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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              ||||||||||||||||
Db       7380 TCTGCCCACAGTACCT 7365


RESULT 3
US-09-949-016-22226
; Sequence 22226, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22226
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-22226

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  Best Local Similarity   93.8%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              |||||||||| |||||
Db         77 TCTGCCCACAATACCT 92


RESULT 4
US-09-949-016-22227
; Sequence 22227, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22227
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-22227

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  Best Local Similarity   93.8%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              |||||||||| |||||
Db         94 TCTGCCCACAATACCT 109


RESULT 5
US-09-949-016-22228
; Sequence 22228, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22228
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-22228

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 601;
  Best Local Similarity   93.8%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCTGCCCACAGTACCT 16
              |||||||||| |||||
Db        464 TCTGCCCACAATACCT 479


RESULT 6
US-09-949-016-22229
; Sequence 22229, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:49:05 ; Search time 1031.35 Seconds
(without alignments)
1157.425 Million cell updates/sec

Title: US-10-754-446-4
Perfect score: 21
Sequence: 1 ctcaccgtgctggaagacact 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
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10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	21	100.0	579	8	AF305572S5	AF305576 Homo sapi
c	2	21	100.0	13270	8	AF287270	AF287270 Homo sapi
	3	21	100.0	155645	14	AC021153	AC021153 Homo sapi
c	4	21	100.0	173126	8	AC008878	AC008878 Homo sapi
c	5	18.4	87.6	1740	6	AX280021	AX280021 Sequence
c	6	18.4	87.6	1829	6	CQ719994	CQ719994 Sequence
c	7	18.4	87.6	2004	8	AF249319	AF249319 Homo sapi
c	8	18.4	87.6	2037	8	HSA293970	AJ293970 Homo sapi
c	9	18.4	87.6	2049	8	AK026102	AK026102 Homo sapi
c	10	18.4	87.6	2051	8	AF287269	AF287269 Homo sapi
c	11	18.4	87.6	2052	6	AX083508	AX083508 Sequence
c	12	18.4	87.6	2063	8	AK222673	AK222673 Homo sapi
c	13	18.4	87.6	2078	8	BC005149	BC005149 Homo sapi
c	14	18.4	87.6	2094	6	BD233734	BD233734 31 human
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c	16	18.4	87.6	2272	8	HSA293659	AJ293659 Homo sapi
c	17	18.4	87.6	165079	14	AC128011	AC128011 Rattus no
c	18	18.4	87.6	195753	14	AC128091	AC128091 Rattus no
	19	18.4	87.6	217148	9	AL773540	AL773540 Mouse DNA
c	20	18.4	87.6	224426	14	AC108247	AC108247 Rattus no
	21	18.4	87.6	234616	14	AC112952	AC112952 Mus muscu
c	22	18.4	87.6	241828	14	AC106575	AC106575 Rattus no
	23	18	85.7	10155	1	AE012227	AE012227 Xanthomon
	24	18	85.7	10446	1	AE011765	AE011765 Xanthomon
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c	26	18	85.7	110000	1	CP000050_35	Continuation (36 o
c	27	17.8	84.8	75511	14	AC153278	AC153278 Bos tauru
	28	17.8	84.8	107113	14	AC142559	AC142559 Takifugu
	29	17.8	84.8	110000	1	AY596297_15	Continuation (16 o
c	30	17.8	84.8	145595	14	AC125926	AC125926 Rattus no
c	31	17.8	84.8	169812	14	AC150169	AC150169 Gallus ga
c	32	17.8	84.8	183916	8	AF111169	AF111169 Homo sapi
c	33	17.8	84.8	186330	8	AC007376	AC007376 Homo sapi
c	34	17.8	84.8	198278	14	AC150063	AC150063 Gallus ga
c	35	17.8	84.8	212150	14	AC130048	AC130048 Rattus no
c	36	17.8	84.8	224635	14	AC094848	AC094848 Rattus no
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c	43	17.4	82.9	1766	6	BD248840	BD248840 47 human
c	44	17.4	82.9	2350	8	AY328894	AY328894 Homo sapi
	45	17.4	82.9	2612	9	AF501309	AF501309 Mus muscu

ALIGNMENTS

RESULT 1
AF305572S5/c
LOCUS AF305572S5 579 bp DNA linear PRI 26-DEC-2000
DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 6 and 7.
ACCESSION AF305576
VERSION AF305576.1 GI:11991202
KEYWORDS .
SEGMENT 5 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
PUBMED 10973263
REFERENCE 2 (bases 1 to 579)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES Location/Qualifiers
source 1. .579
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
exon 129. .225
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ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 579;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTCACCGTGCTGGAAGACACT 21
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Db        527 CTCACCGTGCTGGAAGACACT 507


RESULT 2
AF287270/c
LOCUS       AF287270               13270 bp    DNA     linear   PRI 30-OCT-2000
DEFINITION  Homo sapiens mucolipin (MCOLN1) gene, complete cds.
ACCESSION   AF287270
VERSION     AF287270.1  GI:9844925
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 13270)
  AUTHORS   Sun,M., Goldin,E., Stahl,S., Falardeau,J.L., Kennedy,J.C.,
            Acierno,J.S. Jr., Bove,C., Kaneski,C.R., Nagle,J., Bromley,M.C.,
            Colman,M., Schiffmann,R. and Slaugenhaupt,S.A.
  TITLE     Mucolipidosis type IV is caused by mutations in a gene encoding a
            novel transient receptor potential channel
  JOURNAL   Hum. Mol. Genet. 9 (17), 2471-2478 (2000)
   PUBMED   11030752
REFERENCE   2  (bases 1 to 13270)
  AUTHORS   Slaugenhaupt,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institute
            of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
            Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .13270
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.3"
     gene            1401. .12753
                     /gene="MCOLN1"
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                     12534. .12753)
                     /gene="MCOLN1"
                     /product="mucolipin"
     CDS             join(1526. .1556,3736. .3941,5214. .5381,5536. .5701,
                     6295. .6403,6639. .6735,6933. .7032,7372. .7478,7596. .7745,
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                     12534. .12570)
                     /gene="MCOLN1"
                     /codon_start=1
                     /product="mucolipin"
                     /protein_id="AAG00798.1"
                     /db_xref="GI:9844926"
                     /translation="MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPEEEDLRRR
                     LKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFR
                     HLFLLGYSDGADDTFAAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGDPWTNG
                     SGLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPPSDDLTLLESSSSY
                     KNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLE
                     TQAHIQECKHPSVFQHGDNSFRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFM
                     WRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT
                     STLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPY
                     HVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYM
                     VLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
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ORIGIN

  Query Match           100.0%;  Score 21;  DB 8;  Length 13270;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CTCACCGTGCTGGAAGACACT 21
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Db       7037 CTCACCGTGCTGGAAGACACT 7017


RESULT 3
AC021153
LOCUS       AC021153               155645 bp    DNA     linear   HTG 07-JUL-2000
DEFINITION  Homo sapiens chromosome 19 clone RP11-492L14, WORKING DRAFT
            SEQUENCE, 20 unordered pieces.
ACCESSION   AC021153
VERSION     AC021153.6  GI:8570240
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 155645)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155645)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jun 17, 2000 this sequence version replaced gi:7344405.

            ---------- Genome Center ----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ---------- Project Information ----------
            Center project name: H_NH0492L14
            ---------- Summary Statistics  ----------
            Sequencing vector: M13; 82%
            Sequencing vector: plasmid; 18%
            Chemistry: Dye-primer ET; 77% of reads
            Chemistry: Dye-terminator Big Dye; 23% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 141755 bases at least Q40
            Consensus quality: 145922 bases at least Q30
            Consensus quality: 148291 bases at least Q20
            Insert size: 167000; agarose-fp
            Insert size: 153745; sum-of-contigs
            Quality coverage: 3.76 in Q20 bases; agarose-fp
            Quality coverage: 4.16 in Q20 bases; sum-of-contigs
            ----------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1052: contig of 1052 bp in length
            *     1053     1152: gap of unknown length
            *     1153     2714: contig of 1562 bp in length
            *     2715     2814: gap of unknown length
            *     2815     4101: contig of 1287 bp in length
            *     4102     4201: gap of unknown length
            *     4202     7146: contig of 2945 bp in length
            *     7147     7246: gap of unknown length
            *     7247     9807: contig of 2561 bp in length
            *     9808     9907: gap of unknown length
            *     9908    12944: contig of 3037 bp in length
            *    12945    13044: gap of unknown length
            *    13045    16486: contig of 3442 bp in length
            *    16487    16586: gap of unknown length
            *    16587    20919: contig of 4333 bp in length
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 2348.47 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-4
Perfect score: 21
Sequence: 1 ctcaccgtgctggaagacact 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	21	100.0	868	3	BI909885	BI909885 603070517
c	2	18.4	87.6	225	8	CX226198	CX226198 MBM01462
c	3	18.4	87.6	331	8	Z43611	Z43611 HSC1GD031 n
c	4	18.4	87.6	333	8	T35364	T35364 EST83466 Hu
c	5	18.4	87.6	350	8	Z43604	Z43604 HSC1GA071 n
c	6	18.4	87.6	423	8	H64102	H64102 yr57e02.r1
c	7	18.4	87.6	582	3	BP196543	BP196543 BP196543
c	8	18.4	87.6	818	2	BG831705	BG831705 602765791
c	9	18.4	87.6	826	2	BG913075	BG913075 602806464
c	10	18.4	87.6	873	6	CD558014	CD558014 AGENCOURT
c	11	18.4	87.6	878	5	BQ956452	BQ956452 AGENCOURT
	12	18.4	87.6	901	5	BX433310	BX433310 BX433310
c	13	18.4	87.6	940	5	BU858168	BU858168 AGENCOURT
c	14	18.4	87.6	979	5	BQ918296	BQ918296 AGENCOURT
c	15	18.4	87.6	993	2	BG739714	BG739714 602630410
c	16	18.4	87.6	1078	5	BX362786	BX362786 BX362786
c	17	18.4	87.6	1273	4	CR616477	CR616477 full-leng
c	18	18.4	87.6	1743	10	AY410283	AY410283 Homo sapi
c	19	18.4	87.6	1996	4	CR622331	CR622331 full-leng
	20	18.4	87.6	3287	4	AK048278	AK048278 Mus muscu
	21	18	85.7	901	7	CK159092	CK159092 FGAS04047
c	22	17.8	84.8	539	7	CR927955	CR927955 CR927955
c	23	17.8	84.8	552	3	BI775909	BI775909 468633 MA
c	24	17.8	84.8	604	7	CN791999	CN791999 4126811 B
	25	17.8	84.8	660	9	BZ268910	BZ268910 CH230-421
	26	17.8	84.8	1245	6	CA491046	CA491046 AGENCOURT
	27	17.8	84.8	1658	2	BE962361	BE962361 601655632
c	28	17.4	82.9	219	3	BM293485	BM293485 C0305H01-
	29	17.4	82.9	223	1	AI630095	AI630095 ad02a08.r
	30	17.4	82.9	271	8	N75483	N75483 za83f06.s1
	31	17.4	82.9	276	1	AA330598	AA330598 EST34318
	32	17.4	82.9	283	6	CA880163	CA880163 K0980F07-
	33	17.4	82.9	308	1	AA879907	AA879907 vw01e11.r
	34	17.4	82.9	343	2	BB793665	BB793665 BB793665
	35	17.4	82.9	364	8	H26993	H26993 yo59a12.s1
	36	17.4	82.9	375	5	BU735335	BU735335 UI-E-DW0-
c	37	17.4	82.9	384	8	H42449	H42449 yo10a05.r1
	38	17.4	82.9	388	1	AI689890	AI689890 tx26d03.x
c	39	17.4	82.9	395	2	BE690638	BE690638 uw57a01.x
	40	17.4	82.9	403	11	DE136711	DE136711 Oryzias l
	41	17.4	82.9	409	1	AI190915	AI190915 qd61g04.x
	42	17.4	82.9	415	1	AI061413	AI061413 an29g01.x
	43	17.4	82.9	418	1	AW172705	AW172705 xj02c04.x
	44	17.4	82.9	421	1	AA430026	AA430026 zw65e11.s
	45	17.4	82.9	421	8	N62729	N62729 yz76g05.s1

ALIGNMENTS

RESULT 1
BI909885/c
LOCUS BI909885 868 bp mRNA linear EST 16-OCT-2001
DEFINITION 603070517F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5219237 5', mRNA sequence.
ACCESSION BI909885
VERSION BI909885.1 GI:16173182
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 868)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11551 row: b column: 06
High quality sequence stop: 819.
FEATURES Location/Qualifiers
source 1. .868
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5219237"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH_MGC Library."
ORIGIN

Query Match 100.0%; Score 21; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACCGTGCTGGAAGACACT 21
||||||||||||||||||||
Db 122 CTCACCGTGCTGGAAGACACT 102

RESULT 2
CX226198/c
LOCUS CX226198 225 bp mRNA linear EST 29-DEC-2004
DEFINITION MBM01462 Mus Musculus hematopoietic BM-HPC5 cDNA library Mus musculus cDNA 5', mRNA sequence.
ACCESSION CX226198
VERSION CX226198.1 GI:56881490
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 225)
AUTHORS Williams,C., Wirta,V., Richter,K., Karlsson,C., Lundeberg,J. and Carlsson,L.
TITLE Expressed sequence tags of cDNA clones from a hematopoietic stem cell line expressing Lhx2
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
AlbaNova University Center, KTH-Royal Institute of Technology, 106 91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13REV.
FEATURES Location/Qualifiers
source 1. .225
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6-cast"
/db_xref="taxon:10090"
/sex="Male and Female"
/tissue_type="Bone Marrow"
/cell_type="Hematopoietic progenitor/stem cells immortalized by Lhx2"
/cell_line="hematopoietic stem cell-like cell line BM-HPC5"
/dev_stage="adult"
/clone_lib="Mus Musculus hematopoietic BM-HPC5 cDNA library"
/note="Organ: Bone Marrow; Vector: pCMVSport6.1; Preamplified custom cDNA library by Invitrogen/ResGen"
ORIGIN

Query Match 87.6%; Score 18.4; DB 8; Length 225;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCACCGTGCTGGAAGACAC 20
|||||| ||||||||||||
Db 141 CTCACCATGCTGGAAGACAC 122

RESULT 3
Z43611/c
LOCUS Z43611 331 bp mRNA linear EST 14-NOV-1994
DEFINITION HSC1GD031 normalized infant brain cDNA Homo sapiens cDNA clone c-1gd03, mRNA sequence.
ACCESSION Z43611
VERSION Z43611.1 GI:572807
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 331)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
PUBMED 7757816
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1gd03
Seq primer: (-21)M13_universal.
FEATURES Location/Qualifiers
source 1. .331
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-1gd03"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
ORIGIN

Query Match 87.6%; Score 18.4; DB 8; Length 331;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCACCGTGCTGGAAGACACT 21
|| ||||||||||||||||||
Db 100 TCTCCGTGCTGGAAGACACT 81

RESULT 4
T35364/c
LOCUS T35364 333 bp mRNA linear EST 06-SEP-1995
DEFINITION EST83466 Human Brain Homo sapiens cDNA 5' end similar to None, mRNA sequence.
ACCESSION T35364
VERSION T35364.1 GI:617462
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 333)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 284.928 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-4
Perfect score: 21
Sequence: 1 ctcaccgtgctggaagacact 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	14	AEB28960	Aeb28960 Human MCO
c	2	21	100.0	11365	4	AAK73827	Aak73827 Human imm
c	3	21	100.0	13270	9	ADB84283	Adb84283 Human muc
c	4	21	100.0	20046	4	AAK73826	Aak73826 Human imm
	5	20	95.2	20	9	ADB84282	Adb84282 Human muc
	6	18.4	87.6	1619	4	AAI61022	Aai61022 Human pol
c	7	18.4	87.6	1740	6	AAI71700	Aai71700 Human TRP
c	8	18.4	87.6	1740	6	ABL40755	Abl40755 Human TLC
c	9	18.4	87.6	1741	4	AAI59236	Aai59236 Human pol
c	10	18.4	87.6	1743	9	ADB84284	Adb84284 Human muc
c	11	18.4	87.6	1743	14	ADV66231	Adv66231 TRP-like
c	12	18.4	87.6	2051	13	ADP25150	Adp25150 PRO polyp
c	13	18.4	87.6	2052	4	AAF81753	Aaf81753 Human mem
c	14	18.4	87.6	2092	6	ABL90358	Abl90358 Human pol
c	15	18.4	87.6	2094	3	AAA39067	Aaa39067 Human sec
c	16	18.4	87.6	2095	6	AAI71699	Aai71699 Human TRP
c	17	18.4	87.6	2095	6	ABL40754	Abl40754 Human TLC
c	18	18.4	87.6	2095	14	ADV66229	Adv66229 TRP-like
c	19	18.4	87.6	2140	12	ADQ24925	Adq24925 Human sof
c	20	17.4	82.9	370	5	ABA12621	Aba12621 Human ner
	21	17.4	82.9	421	6	ABN94509	Abn94509 Gene #100
c	22	17.4	82.9	1766	3	AAA78381	Aaa78381 Human sec
c	23	17.4	82.9	1766	8	ADA39925	Ada39925 Human sec
c	24	17.4	82.9	1766	8	ACC50509	Acc50509 Human sec
c	25	17.4	82.9	1766	8	ABZ71282	Abz71282 Secreted
c	26	17.4	82.9	1766	9	ADB91188	Adb91188 Human sec
c	27	17.4	82.9	1766	10	ADC73569	Adc73569 Human sec
c	28	17.4	82.9	1766	10	ADA56112	Ada56112 Gene enco
	29	17.4	82.9	2530	14	AEA47619	Aea47619 Nucleotid
c	30	17.4	82.9	2750	6	ABL92130	Abl92130 Human Tum
c	31	17.4	82.9	2750	10	ABX72055	Abx72055 DNA encod
	32	17.4	82.9	3258	4	AAH42269	Aah42269 Nucleotid
c	33	17.4	82.9	3263	10	ADA53072	Ada53072 Human cod
c	34	17.4	82.9	3272	10	ADE31397	Ade31397 Human dia
c	35	17.4	82.9	3351	11	ACN44967	Acn44967 Human mRN
c	36	17.4	82.9	125534	11	ACN44966	Acn44966 Human gen
c	37	17	81.0	2092	5	AAS72274	Aas72274 DNA encod
	38	16.8	80.0	102	10	ADG25870	Adg25870 INPIONCH0
c	39	16.8	80.0	297	8	ABX43933	Abx43933 Bovine ES
c	40	16.8	80.0	399	8	ABX45303	Abx45303 Bovine ES
c	41	16.8	80.0	433	8	ABX39870	Abx39870 Bovine ES
c	42	16.8	80.0	472	6	ABN73626	Abn73626 Bovine em
c	43	16.8	80.0	586	10	ADD34724	Add34724 Mouse mit
	44	16.8	80.0	594	12	ACH77455	Ach77455 Human gen
	45	16.8	80.0	2988	8	ACA57290	Aca57290 Human adi

ALIGNMENTS

RESULT 1
AEB28960
ID AEB28960 standard; DNA; 21 BP.
XX
AC AEB28960;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene PCR primer PRI R2 SEQ ID NO:4.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 1; SEQ ID NO 4; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a PCR primer for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 21 BP; 5 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACCGTGCTGGAAGACACT 21
||||||||||||||||||||
Db 1 CTCACCGTGCTGGAAGACACT 21

RESULT 2
AAK73827/c
ID AAK73827 standard; DNA; 11365 BP.
XX
AC AAK73827;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-10-754-446-4
Perfect score: 21
Sequence: 1 ctcaccgtgctggaagacact 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	95.2	20	3	US-09-851-494B-11	Sequence 11, Appl
c 4	18.4	87.6	25	10	US-11-060-756-194946	Sequence 194946,
c 5	18.4	87.6	1400	10	US-11-060-756-2850	Sequence 2850, Ap
c 6	18.4	87.6	1400	10	US-11-060-756-7122	Sequence 7122, Ap
c 7	18.4	87.6	1740	3	US-09-828-466-3	Sequence 3, Appli
c 8	18.4	87.6	1740	5	US-10-103-458-3	Sequence 3, Appli
c 9	18.4	87.6	1743	8	US-10-782-695-6	Sequence 6, Appli
c 10	18.4	87.6	2051	3	US-09-851-494B-2	Sequence 2, Appli
c 11	18.4	87.6	2052	3	US-09-965-529-50	Sequence 50, Appl
c 12	18.4	87.6	2052	3	US-09-969-680A-50	Sequence 50, Appl
c 13	18.4	87.6	2052	10	US-11-048-692-50	Sequence 50, Appl
c 14	18.4	87.6	2092	6	US-10-264-237-920	Sequence 920, App
c 15	18.4	87.6	2094	3	US-09-820-893-26	Sequence 26, Appl
c 16	18.4	87.6	2094	7	US-10-607-565-26	Sequence 26, Appl
c 17	18.4	87.6	2095	3	US-09-828-466-1	Sequence 1, Appli
c 18	18.4	87.6	2095	5	US-10-103-458-1	Sequence 1, Appli
c 19	18.4	87.6	2095	8	US-10-782-695-4	Sequence 4, Appli
c 20	18.4	87.6	2140	8	US-10-723-860-7745	Sequence 7745, Ap
21	17.4	82.9	421	3	US-09-880-107-1007	Sequence 1007, Ap
c 22	17.4	82.9	644	5	US-10-027-632-193464	Sequence 193464,
c 23	17.4	82.9	644	6	US-10-027-632-193464	Sequence 193464,
c 24	17.4	82.9	1766	3	US-09-895-298-11	Sequence 11, Appl
c 25	17.4	82.9	1766	8	US-10-885-039-11	Sequence 11, Appl
c 26	17.4	82.9	1766	9	US-10-472-533-103	Sequence 103, App
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c 28	17.4	82.9	2750	3	US-09-918-715-282	Sequence 282, App
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c 30	17.4	82.9	2750	9	US-10-979-159-282	Sequence 282, App
c 31	17.4	82.9	3263	6	US-10-094-749-640	Sequence 640, App
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c 33	17.4	82.9	125534	5	US-10-087-192-1678	Sequence 1678, Ap
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c 35	16.8	80.0	297	3	US-09-960-352-9098	Sequence 9098, Ap
36	16.8	80.0	392	7	US-10-424-599-58115	Sequence 58115, A
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c 38	16.8	80.0	433	3	US-09-960-352-5035	Sequence 5035, Ap
c 39	16.8	80.0	472	3	US-09-876-143-565	Sequence 565, App
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c 45	16.8	80.0	462586	9	US-10-476-264-420	Sequence 420, App

ALIGNMENTS

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; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-754-446-4

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTCACCGTGCTGGAAGACACT 21

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; Sequence 1, Application US/09851494B
; Publication No. US20030064363A1
; GENERAL INFORMATION:
; APPLICANT: ML4 Foundation
; APPLICANT: Goldin, Ehud
; APPLICANT: Slaugenhaupt, Susan A.
; APPLICANT: Sun, Mei
; APPLICANT: Acierno, James S.
; TITLE OF INVENTION: A Gene Encoding A New TRP Channel is Mutated in Mucolipidosis IV
; FILE REFERENCE: 3394/1H557US1
; CURRENT APPLICATION NUMBER: US/09/851,494B
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 11

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; SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-494B-1

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; Publication No. US20030064363A1
; GENERAL INFORMATION:
;  APPLICANT: ML4 Foundation
;  APPLICANT:  Goldin, Ehud
;  APPLICANT:  Slaugenhaupt, Susan A.
;  APPLICANT:  Sun, Mei
;  APPLICANT:  Acierno, James S.
;  TITLE OF INVENTION: A Gene Encoding A New TRP Channel is Mutated in Mucolipidosis IV
;  FILE REFERENCE: 3394/1H557US1
;  CURRENT APPLICATION NUMBER: US/09/851,494B
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 11
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-851-494B-11

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; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
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;   TYPE: DNA
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US-11-060-756-194946

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; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
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US-11-060-756-2850

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; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7122
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;   ORGANISM: Homo sapiens
US-11-060-756-7122

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; Patent No. US20020035056A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Immaculada
;  TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
;  FILE REFERENCE: MNI-125CP
;  CURRENT APPLICATION NUMBER: US/09/828,466
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	5	15.4	73.3	1238	6	US-10-821-234-1	Sequence 1, Appli
	6	15.4	73.3	1244	7	US-11-000-688-733	Sequence 733, App
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	8	15.4	73.3	175673	7	US-11-121-086-55	Sequence 55, Appl
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c	11	15.2	72.4	579	7	US-11-128-061-3984	Sequence 3984, Ap
c	12	15.2	72.4	866	6	US-10-750-185-61786	Sequence 61786, A
c	13	15.2	72.4	866	6	US-10-750-623-61786	Sequence 61786, A
	14	15.2	72.4	1008	6	US-10-750-185-54439	Sequence 54439, A
	15	15.2	72.4	1008	6	US-10-750-623-54439	Sequence 54439, A
c	16	15.2	72.4	1077	6	US-10-517-939-369	Sequence 369, App
	17	15.2	72.4	1307	6	US-10-750-185-27270	Sequence 27270, A
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c	19	15.2	72.4	1350	7	US-11-055-822-289	Sequence 289, App
c	20	15.2	72.4	3272	6	US-10-750-185-24646	Sequence 24646, A
c	21	15.2	72.4	3272	6	US-10-750-623-24646	Sequence 24646, A
c	22	15.2	72.4	4730	7	US-11-128-061-520	Sequence 520, App
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	30	14.8	70.5	19	9	US-11-083-784-285326	Sequence 285326,
	31	14.8	70.5	25	7	US-11-121-849-182614	Sequence 182614,
c	32	14.8	70.5	201	6	US-10-995-561-23969	Sequence 23969, A
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c	36	14.8	70.5	1388	7	US-11-128-061-969	Sequence 969, App
	37	14.8	70.5	1481	7	US-11-000-688-788	Sequence 788, App
c	38	14.8	70.5	1646	6	US-10-750-185-55975	Sequence 55975, A
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	42	14.8	70.5	127340	7	US-11-112-908-35	Sequence 35, Appl
	43	14.8	70.5	207835	7	US-11-121-086-39	Sequence 39, Appl
	44	14.8	70.5	207835	7	US-11-121-086-40	Sequence 40, Appl
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; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
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; SEQ ID NO 2907
; LENGTH: 77246
; TYPE: DNA
; ORGANISM: Homo sapiens
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; LOCATION: 10718, 10719, 10720, 10721, 10722, 10723, 10724, 10725, 10726,
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; LOCATION: 10743, 10744, 10745, 10746, 10747, 10748, 10749, 10750
; OTHER INFORMATION: n = A,T,C or G
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; LOCATION: 10760, 10761, 10762, 10763, 10764, 10765, 10766, 10767,
; LOCATION: 10768, 10769, 10770, 10771, 10772, 10773, 10774, 10775,
; LOCATION: 10776, 10777, 10778, 10779, 10780, 10781, 10782, 10783
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10784, 10785, 10786, 10787, 10788, 10789, 10790, 10791, 10792,
; LOCATION: 10793, 10794, 10795, 10796, 10797, 10798, 10799, 10800,
; LOCATION: 10801, 10802, 10803, 10804, 10805, 10806, 10807, 10808,
; LOCATION: 10809, 10810, 10811, 10812, 10813, 10814, 10815, 10816
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature

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;   LOCATION: 10817, 10818, 10819, 10820, 10821, 10822, 10823, 10824, 10825,
;   LOCATION: 10826, 10827, 10828, 10829, 10830, 10831, 10832, 10833,
;   LOCATION: 10834, 10835, 10836, 10837, 10838, 10839, 10840, 10841,
;   LOCATION: 10842, 10843, 10844, 10845, 10846, 10847, 10848, 10849
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10850, 10851, 10852, 10853, 10854, 10855, 10856, 10857, 10858,
;   LOCATION: 10859, 10860, 10861, 10862, 10863, 10864, 10865, 10866,
;   LOCATION: 10867, 10868, 10869, 10870, 10871, 10872, 10873, 10874,
;   LOCATION: 10875, 10876, 10877, 10878, 10879, 10880, 10881, 10882
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10883, 10884, 10885, 10886, 10887, 10888, 10889, 10890, 10891,
;   LOCATION: 10892, 10893, 10894, 10895, 10896, 10897, 10898, 10899,
;   LOCATION: 10900, 10901, 10902, 10903, 10904, 10905, 10906, 10907,
;   LOCATION: 10908, 10909, 10910, 10911, 10912, 10913, 10914, 10915
;   OTHER INFORMATION: n = A,T,C or G
US-11-124-368A-2907

  Query Match             77.1%;  Score 16.2;  DB 7;  Length 77246;
  Best Local Similarity   85.7%;  Pred. No. 77;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTCACCGTGCTGGAAGACACT 21
              |||||| ||| ||| ||||||
Db        633 CTCACCCTGCAGGAGGACACT 653


RESULT 2
US-10-995-561-13352/c
; Sequence 13352, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13352
;   LENGTH: 32157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13352

  Query Match             75.2%;  Score 15.8;  DB 6;  Length 32157;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TCACCGTGCTGGAAGACAC 20
              |||||||| ||||||| ||
Db      17401 TCACCGTGGTGGAAGAAAC 17383


RESULT 3
US-11-101-244-151656
; Sequence 151656, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 151656
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-151656

  Query Match             73.3%;  Score 15.4;  DB 8;  Length 19;
  Best Local Similarity   76.5%;  Pred. No. 1.3e+02;
  Matches   13;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCACCGTGCTGGAAGAC 18
              :|| ||:||:|||||||
Db          1 UCAACGUGCUGGAAGAC 17


RESULT 4
US-11-083-784-151656
; Sequence 151656, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 151656
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-151656

  Query Match             73.3%;  Score 15.4;  DB 9;  Length 19;
  Best Local Similarity   76.5%;  Pred. No. 1.3e+02;
  Matches   13;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCACCGTGCTGGAAGAC 18
              :|| ||:||:|||||||
Db          1 UCAACGUGCUGGAAGAC 17


RESULT 5
US-10-821-234-1
; Sequence 1, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:32:47 ; Search time 76.44 Seconds
(without alignments)
488.341 Million cell updates/sec

Title: US-10-754-446-4
Perfect score: 21
Sequence: 1 ctcaccgtgctggaagacact 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	21	100.0	601	3	US-09-949-016-59085	Sequence 59085, A
c	2	21	100.0	15353	3	US-09-949-016-13454	Sequence 13454, A
c	3	18.4	87.6	2051	3	US-09-949-016-1712	Sequence 1712, Ap
	4	16.2	77.1	25	3	US-09-396-196G-50417	Sequence 50417, A
c	5	16.2	77.1	471	3	US-09-270-767-1970	Sequence 1970, Ap
c	6	16.2	77.1	471	3	US-09-270-767-17252	Sequence 17252, A
	7	16.2	77.1	601	3	US-09-949-016-178570	Sequence 178570,
	8	16.2	77.1	601	3	US-09-949-016-178571	Sequence 178571,
	9	16.2	77.1	797	3	US-09-270-767-7266	Sequence 7266, Ap
	10	16.2	77.1	797	3	US-09-270-767-22548	Sequence 22548, A
	11	16.2	77.1	3385	3	US-09-509-800-1	Sequence 1, Appli
c	12	16.2	77.1	12470	3	US-09-949-002-847	Sequence 847, App
c	13	16.2	77.1	17896	3	US-09-949-016-16867	Sequence 16867, A
	14	16.2	77.1	32665	3	US-09-949-016-14098	Sequence 14098, A
	15	16.2	77.1	52667	3	US-09-949-016-12019	Sequence 12019, A
	16	16.2	77.1	141560	3	US-09-949-016-16476	Sequence 16476, A
	17	15.8	75.2	25	3	US-09-396-196G-50406	Sequence 50406, A
	18	15.8	75.2	659	3	US-09-533-559-6889	Sequence 6889, Ap
	19	15.8	75.2	1293	3	US-09-902-540-5426	Sequence 5426, Ap
c	20	15.8	75.2	24154	3	US-09-949-016-16374	Sequence 16374, A
c	21	15.8	75.2	27465	3	US-09-949-016-16561	Sequence 16561, A
c	22	15.8	75.2	34953	3	US-09-902-540-1263	Sequence 1263, Ap
	23	15.4	73.3	358	3	US-09-513-999C-3422	Sequence 3422, Ap
c	24	15.4	73.3	601	3	US-09-949-016-51396	Sequence 51396, A
	25	15.4	73.3	624	3	US-09-513-999C-2084	Sequence 2084, Ap
	26	15.4	73.3	717	3	US-09-949-002-92	Sequence 92, Appl
	27	15.4	73.3	717	3	US-09-949-002-127	Sequence 127, App
	28	15.4	73.3	1037	2	US-08-240-124-1	Sequence 1, Appli
	29	15.4	73.3	1037	2	US-08-453-943-1	Sequence 1, Appli
	30	15.4	73.3	1037	2	US-09-057-121-1	Sequence 1, Appli
	31	15.4	73.3	1037	3	US-09-358-734-1	Sequence 1, Appli
	32	15.4	73.3	1037	3	US-09-904-954-1	Sequence 1, Appli
	33	15.4	73.3	1070	2	US-08-299-567-8	Sequence 8, Appli
	34	15.4	73.3	1092	2	US-08-646-590B-35	Sequence 35, Appl
	35	15.4	73.3	1092	3	US-09-412-184-35	Sequence 35, Appl
	36	15.4	73.3	1212	3	US-09-949-016-1491	Sequence 1491, Ap
	37	15.4	73.3	1374	3	US-09-902-540-4675	Sequence 4675, Ap
	38	15.4	73.3	1533	3	US-09-711-164-194	Sequence 194, App
	39	15.4	73.3	2646	3	US-09-489-039A-4832	Sequence 4832, Ap
c	40	15.4	73.3	6503	3	US-09-404-650-12	Sequence 12, Appl
c	41	15.4	73.3	6503	3	US-09-935-541-12	Sequence 12, Appl
c	42	15.4	73.3	6503	3	US-10-425-800-12	Sequence 12, Appl
c	43	15.4	73.3	6816	3	US-09-404-650-1	Sequence 1, Appli
c	44	15.4	73.3	6816	3	US-09-935-541-1	Sequence 1, Appli
c	45	15.4	73.3	6816	3	US-10-425-800-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-59085/c
; Sequence 59085, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59085
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59085

Query Match 100.0%; Score 21; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTCACCGTGCTGGAAGACACT 21
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Db        504 CTCACCGTGCTGGAAGACACT 484
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RESULT 2
US-09-949-016-13454/c
; Sequence 13454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13454
;   LENGTH: 15353
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13454

  Query Match            100.0%;  Score 21;  DB 3;  Length 15353;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCACCGTGCTGGAAGACACT 21
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Db       7637 CTCACCGTGCTGGAAGACACT 7617


RESULT 3
US-09-949-016-1712/c
; Sequence 1712, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1712
;   LENGTH: 2051
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1712

  Query Match             87.6%;  Score 18.4;  DB 3;  Length 2051;
  Best Local Similarity   95.0%;  Pred. No. 20;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCACCGTGCTGGAAGACACT 21
              || ||||||||||||||||||
Db       1006 TCTCCGTGCTGGAAGACACT 987


RESULT 4
US-09-396-196G-50417
; Sequence 50417, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50417
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-50417

  Query Match             77.1%;  Score 16.2;  DB 3;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTCACCGTGCTGGAAGACACT 21
              | || ||||||||||||||| |
Db          4 CACAACGTGCTGGAAGACAGT 24


RESULT 5
US-09-270-767-1970/c
; Sequence 1970, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1970
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-1970

  Query Match             77.1%;  Score 16.2;  DB 3;  Length 471;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTCACCGTGCTGGAAGACACT 21
              || |||||||||| |||| |
Db        451 CTGACCGTGCTGGACGACAGT 431


RESULT 6
US-09-270-767-17252/c
; Sequence 17252, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17252
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-17252

  Query Match             77.1%;  Score 16.2;  DB 3;  Length 471;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTCACCGTGCTGGAAGACACT 21
              || |||||||||| |||| |
Db        451 CTGACCGTGCTGGACGACAGT 431


RESULT 7
US-09-949-016-178570
; Sequence 178570, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:49:05 ; Search time 982.24 Seconds
(without alignments)
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Title: US-10-754-446-3
Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_in:*
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4: gb_om:*
5: gb_ov:*
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8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match %	Length	DB	ID	Description
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c	2	20	100.0	51	6	AX199337	AX199337 Sequence
c	3	20	100.0	51	6	AX199338	AX199338 Sequence
	4	20	100.0	71	6	AX522607	AX522607 Sequence
c	5	20	100.0	77	6	AX523183	AX523183 Sequence
c	6	20	100.0	98	6	BD039678	BD039678 Sequence
c	7	20	100.0	98	6	AX904145	AX904145 Sequence
	8	20	100.0	102	6	BD037012	BD037012 Sequence
	9	20	100.0	102	6	AX901479	AX901479 Sequence
c	10	20	100.0	107	6	CQ685626	CQ685626 Sequence
c	11	20	100.0	108	6	CQ694139	CQ694139 Sequence
c	12	20	100.0	114	6	BD044993	BD044993 Sequence
c	13	20	100.0	114	6	AX909460	AX909460 Sequence
	14	20	100.0	117	6	BD037394	BD037394 Sequence
c	15	20	100.0	117	6	BD044139	BD044139 Sequence
	16	20	100.0	117	6	AX901861	AX901861 Sequence
c	17	20	100.0	117	6	AX908606	AX908606 Sequence
	18	20	100.0	128	6	BD034714	BD034714 Sequence
	19	20	100.0	128	6	AX899181	AX899181 Sequence
c	20	20	100.0	129	6	CQ708055	CQ708055 Sequence
	21	20	100.0	145	6	BD035848	BD035848 Sequence
	22	20	100.0	145	6	BD045580	BD045580 Sequence
c	23	20	100.0	145	6	BD118446	BD118446 EST and e
c	24	20	100.0	145	6	AR422893	AR422893 Sequence
	25	20	100.0	145	6	AX900315	AX900315 Sequence
	26	20	100.0	145	6	AX910047	AX910047 Sequence
c	27	20	100.0	145	6	AX983587	AX983587 Sequence
c	28	20	100.0	147	6	CQ686625	CQ686625 Sequence
	29	20	100.0	151	6	BD043797	BD043797 Sequence
	30	20	100.0	151	6	AX908264	AX908264 Sequence
c	31	20	100.0	152	6	BD115706	BD115706 EST and e
c	32	20	100.0	152	6	BD117639	BD117639 EST and e
c	33	20	100.0	152	6	AR420153	AR420153 Sequence
c	34	20	100.0	152	6	AR422086	AR422086 Sequence
c	35	20	100.0	152	6	AX980847	AX980847 Sequence
c	36	20	100.0	152	6	AX982780	AX982780 Sequence
	37	20	100.0	154	10	AB134303	AB134303 Homo sapi
c	38	20	100.0	155	6	BD049251	BD049251 Sequence
c	39	20	100.0	155	6	AX913718	AX913718 Sequence
c	40	20	100.0	158	6	BD115744	BD115744 EST and e
c	41	20	100.0	158	6	BD116463	BD116463 EST and e
c	42	20	100.0	158	6	AR420191	AR420191 Sequence
c	43	20	100.0	158	6	AR420910	AR420910 Sequence
c	44	20	100.0	158	6	AX980885	AX980885 Sequence
c	45	20	100.0	158	6	AX981604	AX981604 Sequence

ALIGNMENTS

RESULT 1
AX163311/c
LOCUS AX163311 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6639 from Patent WO0140521.
ACCESSION AX163311
VERSION AX163311.1 GI:14544642
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6639 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (6640 is other entry)
Accession number cg38821538"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGTTGCCCAGGCT 20
||||||||||||||||||||
Db 37 CTTGCTCTGTTGCCCAGGCT 18

RESULT 2
AX199337/c
LOCUS AX199337 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 267 from Patent WO0151670.

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ACCESSION   AX199337
VERSION     AX199337.1  GI:15389718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.D.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0151670-A 267 19-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (268 is other entry)
                     Accession number cg43011316"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         49 CTTGCTCTGTTGCCCAGGCT 30


RESULT 3
AX199338/c
LOCUS       AX199338                 51 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 268 from Patent WO0151670.
ACCESSION   AX199338
VERSION     AX199338.1  GI:15389719
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.D.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0151670-A 268 19-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="2 of 2 allelic variants (267 is other entry)
                     Accession number cg43011316"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         49 CTTGCTCTGTTGCCCAGGCT 30


RESULT 4
AX522607
LOCUS       AX522607                 71 bp    DNA     linear   PAT 24-OCT-2002
DEFINITION  Sequence 277 from Patent WO02064731.
ACCESSION   AX522607
VERSION     AX522607.1  GI:24411561
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R., Tuijnder,M. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02064731-A 277 22-AUG-2002;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         11 CTTGCTCTGTTGCCCAGGCT 30


RESULT 5
AX523183/c
LOCUS       AX523183                 77 bp    DNA     linear   PAT 24-OCT-2002
DEFINITION  Sequence 853 from Patent WO02064731.
ACCESSION   AX523183
VERSION     AX523183.1  GI:24412137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R., Tuijnder,M. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02064731-A 853 22-AUG-2002;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         39 CTTGCTCTGTTGCCCAGGCT 20


RESULT 6
BD039678/c
LOCUS       BD039678                 98 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD039678
VERSION     BD039678.1  GI:22581420
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 2236.64 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-3
Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	38	1	AA054107	AA054107 zf50f06.r
	2	20	100.0	39	1	AA911358	AA911358 oe76d10.s
	3	20	100.0	46	9	AZ576121	AZ576121 AST-T32E0
c	4	20	100.0	49	5	C20875	C20875 HUMGS000494
	5	20	100.0	50	1	AI708455	AI708455 as97e06.x
	6	20	100.0	50	1	AU102403	AU102403 AU102403
	7	20	100.0	52	1	AA903439	AA903439 ok48h04.s
	8	20	100.0	61	1	AI735552	AI735552 at17e12.x
	9	20	100.0	64	1	AW304187	AW304187 xv61e11.x
c	10	20	100.0	68	9	AZ537585	AZ537585 AST-2P881
	11	20	100.0	69	1	AA215549	AA215549 zr97e12.r
c	12	20	100.0	70	1	AA604042	AA604042 no44h11.s
	13	20	100.0	82	2	BG236597	BG236597 nai45g03.
	14	20	100.0	84	9	AZ757146	AZ757146 ew06c09.r
	15	20	100.0	101	1	AA262246	AA262246 zs26e09.s
c	16	20	100.0	102	6	CD640446	CD640446 AGENCOURT
c	17	20	100.0	106	2	BF875905	BF875905 RC3-ET013
	18	20	100.0	108	2	BE141837	BE141837 IL5-HT011
c	19	20	100.0	108	8	T58114	T58114 yb26d03.r1
	20	20	100.0	111	2	BE246735	BE246735 TCBAP1D44
	21	20	100.0	111	9	B66475	B66475 CIT-HSP-201
	22	20	100.0	113	1	AW780390	AW780390 ho05a12.x
c	23	20	100.0	116	3	BQ372956	BQ372956 CM3-FT010
c	24	20	100.0	116	6	CD521979	CD521979 AGENCOURT
c	25	20	100.0	116	8	N83678	N83678 KK2199F Hum
c	26	20	100.0	118	1	AA004455	AA004455 zh89d01.s
c	27	20	100.0	118	8	H57636	H57636 yr21c07.r1
c	28	20	100.0	120	1	AA007673	AA007673 zh99h04.r
	29	20	100.0	120	1	AA013351	AA013351 ze28g12.s
c	30	20	100.0	120	1	AA367235	AA367235 EST78313
	31	20	100.0	122	2	BG956764	BG956764 IL3-CT067
	32	20	100.0	122	2	BG957876	BG957876 IL3-CT067
	33	20	100.0	122	2	BG957892	BG957892 IL3-CT067
c	34	20	100.0	123	7	CK854800	CK854800 SWWbL3CAW
	35	20	100.0	123	8	R92902	R92902 yt71d10.r1
c	36	20	100.0	125	2	BF820510	BF820510 MR1-RT003
c	37	20	100.0	125	8	H71447	H71447 ys08g12.r1
c	38	20	100.0	125	8	H73044	H73044 ys10d07.r1
c	39	20	100.0	125	8	H73847	H73847 ys11f04.r1
	40	20	100.0	126	1	AA579709	AA579709 nm80g02.s
	41	20	100.0	126	9	AQ201947	AQ201947 RPCI11-48
c	42	20	100.0	128	1	AA328830	AA328830 EST32365
c	43	20	100.0	128	8	H67228	H67228 yu65e02.r1
c	44	20	100.0	128	8	T83695	T83695 yd65c07.r1
	45	20	100.0	130	1	AA659815	AA659815 nv02e07.s

ALIGNMENTS

RESULT 1
AA054107/c
LOCUS AA054107 38 bp mRNA linear EST 13-SEP-1996
DEFINITION zf50f06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380387 5' similar to gb:X77738_rna1 BAND 3 ANION TRANSPORT PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA054107
VERSION AA054107.1 GI:1545030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .38
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1288644"
/db_xref="taxon:9606"
/clone="IMAGE:380387"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"

/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGTTGCCCAGGCT 20
||||||||||||||||||||
Db 28 CTTGCTCTGTTGCCCAGGCT 9

RESULT 2
AA911358
LOCUS AA911358 39 bp mRNA linear EST 21-APR-1998
DEFINITION oe76d10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417555 3' similar to gb:X01057_rna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains element MER22 repetitive element ;, mRNA sequence.
ACCESSION AA911358
VERSION AA911358.1 GI:3050722
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 39)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 454 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1417555"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGTTGCCCAGGCT 20
||||||||||||||||||||
Db 8 CTTGCTCTGTTGCCCAGGCT 27

RESULT 3
AZ576121
LOCUS AZ576121 46 bp DNA linear GSS 06-DEC-2000
DEFINITION AST-T32E0027 Genetrap T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
ACCESSION AZ576121
VERSION AZ576121.1 GI:11562432
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .46
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
/note="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGTTGCCCAGGCT 20
||||||||||||||||||||
Db 6 CTTGCTCTGTTGCCCAGGCT 25

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 271.36 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-3
Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	14	AEB28959	Aeb28959 Human MCO
c	2	20	100.0	24	6	ABV75668	Abv75668 Human FD1
	3	20	100.0	41	4	AAH48082	Aah48082 Ras GTPas
c	4	20	100.0	41	6	AAS15951	Aas15951 Human pro
c	5	20	100.0	41	6	AAS15950	Aas15950 Human pro
	6	20	100.0	41	10	ADC59511	Adc59511 Polypepti
c	7	20	100.0	51	4	AAI79698	Aai79698 Human con
c	8	20	100.0	51	4	AAH89487	Aah89487 Human cod
c	9	20	100.0	51	4	AAH89486	Aah89486 Human cod
	10	20	100.0	60	10	ADI20565	Adi20565 Oligonucl
	11	20	100.0	71	8	ABZ09117	Abz09117 Human oli
	12	20	100.0	71	10	ABZ78570	Abz78570 Tumour su
c	13	20	100.0	77	8	ABZ09693	Abz09693 Human oli
c	14	20	100.0	77	10	ABZ79146	Abz79146 Tumour su
	15	20	100.0	82	13	ADR16680	Adr16680 MicroRNA
	16	20	100.0	84	4	AAS28538	Aas28538 Genomic s
	17	20	100.0	84	10	ADG41734	Adg41734 Human res
	18	20	100.0	84	11	ADI97508	Adi97508 Human res
c	19	20	100.0	91	2	AAT26410	Aat26410 Human gen
c	20	20	100.0	93	4	AAK65580	Aak65580 Human imm
c	21	20	100.0	94	4	AAK73464	Aak73464 Human imm
c	22	20	100.0	94	4	AAK72995	Aak72995 Human imm
	23	20	100.0	95	4	AAK77204	Aak77204 Human imm
	24	20	100.0	95	4	AAK77203	Aak77203 Human imm
c	25	20	100.0	95	4	AAK70695	Aak70695 Human imm
c	26	20	100.0	98	3	AAC15933	Aac15933 Human sec
c	27	20	100.0	98	4	AAS36698	Aas36698 Human car
c	28	20	100.0	98	4	AAK71993	Aak71993 Human imm
c	29	20	100.0	98	10	ADE47392	Ade47392 Human car
c	30	20	100.0	98	13	ADJ08810	Adj08810 Human car
	31	20	100.0	102	3	AAC13267	Aac13267 Human sec
c	32	20	100.0	102	4	AAS36278	Aas36278 Human car
c	33	20	100.0	102	10	ADE46972	Ade46972 Human car
c	34	20	100.0	102	13	ADJ08390	Adj08390 Human car
c	35	20	100.0	103	4	AAS28603	Aas28603 Genomic s
c	36	20	100.0	103	10	ADG41799	Adg41799 Human res
c	37	20	100.0	103	11	ADI97573	Adi97573 Human res
c	38	20	100.0	104	4	AAL07415	Aal07415 Human rep
c	39	20	100.0	104	5	AAS40769	Aas40769 DNA encod
c	40	20	100.0	104	11	ADJ09975	Adj09975 Human pro
c	41	20	100.0	106	12	ADO57414	Ado57414 DNA encod
c	42	20	100.0	111	4	AAK74404	Aak74404 Human imm
c	43	20	100.0	113	5	ABA13542	Aba13542 Human ner
c	44	20	100.0	114	3	AAC21248	Aac21248 Human sec
c	45	20	100.0	114	4	AAK77447	Aak77447 Human imm

ALIGNMENTS

RESULT 1
AEB28959
ID AEB28959 standard; DNA; 20 BP.
XX
AC AEB28959;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene PCR primer PRI F1 SEQ ID NO:3.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 1; SEQ ID NO 3; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

```
CC   fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC   described: (1) an oligonucleotide (ON1) comprising a sequence
CC   complementary to the coding or non-coding strand of the mucolipin-1
CC   (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC   sequences, comprising ON1. (M1) is useful for determining the presence of
CC   ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC   is useful for genetic counseling of individuals at risk for ML IV or at
CC   risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC   on chromosome 19p13. The present sequence represents a PCR primer for the
CC   MCOLN1 gene, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db          1 CTTGCTCTGTTGCCCAGGCT 20


RESULT 2
ABV75668/c
ID   ABV75668 standard; DNA; 24 BP.
XX
AC   ABV75668;
XX
DT   28-JAN-2003  (first entry)
XX
DE   Human FD16.06 PCR primer 2.
XX
KW   Human; FD16.06; cancer; HIV; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1351034-A.
XX
PD   29-MAY-2002.
XX
PF   26-OCT-2000; 2000CN-00125785.
XX
PR   26-OCT-2000; 2000CN-00125785.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-619857/67.
XX
PT   Polypeptide-human FD16.06 and polynucleotide for coding it, useful for
PT   treating diseases such as cancer and HIV infection.
XX
PS   Example 2; Page 16 (Disclosure); 33pp; Chinese.
XX
CC   The invention relates to a novel polypeptide, human FD16.06, and the
CC   polynucleotide encoding it. The antagonist against the polypeptide is
CC   also disclosed. The polypeptide is useful for treating diseases such as
CC   cancer and HIV infection. The present sequence represents a PCR primer
CC   used to amplify the human FD16.06 gene of the invention
XX
SQ   Sequence 24 BP; 9 A; 7 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 6;  Length 24;
  Best Local Similarity 100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         22 CTTGCTCTGTTGCCCAGGCT 3


RESULT 3
AAH48082
ID   AAH48082 standard; DNA; 41 BP.
XX
AC   AAH48082;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Ras GTPase-activating protein 12 probe #2.
XX
KW   Ras GTPase-activating protein 12; cytostatic; Antiinflammatory;
KW   Immunomodulatory; Anti-HIV; malignant tumour; haemopathy; HIV infection;
KW   immunological disease; inflammation; gene therapy; probe; ss.
XX
OS   Unidentified.
XX
PN   WO200147998-A1.
XX
PD   05-JUL-2001.
XX
PF   25-DEC-2000; 2000WO-CN000680.
XX
PR   27-DEC-1999;   99CN-00125367.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-418231/44.
XX
PT   RAS GTPase-activating protein 12 and encoded polynucleotide, applicable
PT   in diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT   immunological diseases and various inflammation.
XX
PS   Example 7; Page 20; 38pp; Chinese.
XX
CC   The present invention relates to Ras GTPase-activating protein 12 and its
CC   coding sequence (see AAH48076 and AAG64227). The GTPase-activating
CC   protein and its coding sequence are useful in the diagnosis and treatment
CC   of malignant tumour, haemopathy, HIV infection, immunological diseases
CC   and various inflammations. The present sequence is a probe, which was
CC   used in an example from the present invention
XX
SQ   Sequence 41 BP; 6 A; 10 C; 12 G; 13 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 4;  Length 41;
  Best Local Similarity 100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         13 CTTGCTCTGTTGCCCAGGCT 32


RESULT 4
AAS15951/c
ID   AAS15951 standard; DNA; 41 BP.
XX
AC   AAS15951;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human proteolytic enzyme regulatory protein 11, probe #2.
XX
KW   Human; proteolytic enzyme regulatory protein 11; cytostatic; virucidal;
KW   immunomodulatory; antiinflammatory; haemostatic; cancer; haemopathy;
KW   human immunodeficiency virus; HIV; immunological disease; inflammation;
KW   embryonic development disorder; developmental disorder; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200174867-A1.
XX
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 483.04 Seconds
(without alignments)
342.389 Million cell updates/sec

Title: US-10-754-446-3
Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	9	US-10-754-446-3	Sequence 3, Appli
	2	20	100.0	60	8	US-10-804-859-55	Sequence 55, Appl
	3	20	100.0	71	9	US-10-467-851-277	Sequence 277, App
c	4	20	100.0	72	9	US-10-708-204-6674	Sequence 6674, Ap
c	5	20	100.0	77	9	US-10-467-851-853	Sequence 853, App
c	6	20	100.0	78	9	US-10-708-204-6268	Sequence 6268, Ap
c	7	20	100.0	78	9	US-10-708-204-6998	Sequence 6998, Ap
c	8	20	100.0	83	9	US-10-708-204-6598	Sequence 6598, Ap
	9	20	100.0	84	3	US-09-764-860-972	Sequence 972, App
	10	20	100.0	84	5	US-10-074-095-972	Sequence 972, App
	11	20	100.0	84	6	US-10-212-872-972	Sequence 972, App
c	12	20	100.0	84	9	US-10-708-204-6304	Sequence 6304, Ap
c	13	20	100.0	86	9	US-10-708-204-5760	Sequence 5760, Ap
c	14	20	100.0	87	9	US-10-708-204-6688	Sequence 6688, Ap
c	15	20	100.0	88	9	US-10-708-204-6366	Sequence 6366, Ap
c	16	20	100.0	88	9	US-10-708-204-6626	Sequence 6626, Ap
c	17	20	100.0	88	9	US-10-708-204-6671	Sequence 6671, Ap
c	18	20	100.0	88	9	US-10-708-204-6676	Sequence 6676, Ap
c	19	20	100.0	88	9	US-10-708-204-6689	Sequence 6689, Ap
c	20	20	100.0	88	9	US-10-708-204-6699	Sequence 6699, Ap
c	21	20	100.0	88	9	US-10-708-204-6784	Sequence 6784, Ap
c	22	20	100.0	90	9	US-10-708-204-6710	Sequence 6710, Ap
c	23	20	100.0	92	9	US-10-708-204-6788	Sequence 6788, Ap
c	24	20	100.0	93	9	US-10-708-204-6492	Sequence 6492, Ap
c	25	20	100.0	94	9	US-10-708-204-6445	Sequence 6445, Ap
c	26	20	100.0	95	9	US-10-708-204-6753	Sequence 6753, Ap
c	27	20	100.0	95	9	US-10-708-204-6848	Sequence 6848, Ap
c	28	20	100.0	96	9	US-10-708-204-5730	Sequence 5730, Ap
c	29	20	100.0	96	9	US-10-708-204-6816	Sequence 6816, Ap
c	30	20	100.0	97	9	US-10-708-204-6419	Sequence 6419, Ap
c	31	20	100.0	98	3	US-09-764-869-2198	Sequence 2198, Ap
c	32	20	100.0	98	5	US-10-091-504-2198	Sequence 2198, Ap
c	33	20	100.0	98	6	US-10-227-577-2198	Sequence 2198, Ap
c	34	20	100.0	98	9	US-10-708-204-6436	Sequence 6436, Ap
c	35	20	100.0	99	9	US-10-708-204-5772	Sequence 5772, Ap
c	36	20	100.0	99	9	US-10-708-204-6371	Sequence 6371, Ap
c	37	20	100.0	99	9	US-10-708-204-6374	Sequence 6374, Ap
c	38	20	100.0	99	9	US-10-708-204-6437	Sequence 6437, Ap
c	39	20	100.0	101	9	US-10-708-204-7165	Sequence 7165, Ap
c	40	20	100.0	102	3	US-09-764-869-1778	Sequence 1778, Ap
c	41	20	100.0	102	5	US-10-091-504-1778	Sequence 1778, Ap
c	42	20	100.0	102	6	US-10-227-577-1778	Sequence 1778, Ap
c	43	20	100.0	103	3	US-09-764-860-1037	Sequence 1037, Ap
c	44	20	100.0	103	5	US-10-074-095-1037	Sequence 1037, Ap
c	45	20	100.0	103	6	US-10-212-872-1037	Sequence 1037, Ap

ALIGNMENTS

RESULT 1
US-10-754-446-3
; Sequence 3, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-754-446-3

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGTTGCCCAGGCT 20
||||||||||||||||||||
Db 1 CTTGCTCTGTTGCCCAGGCT 20

RESULT 2
US-10-804-859-55
; Sequence 55, Application US/10804859
; Publication No. US20040265865A1
; GENERAL INFORMATION:
; APPLICANT: The University of Queensland
; TITLE OF INVENTION: A method for identifying effector molecules for gene network inte
; FILE REFERENCE: 2563972/EJH
; CURRENT APPLICATION NUMBER: US/10/804,859
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/324127
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55

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;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: human
US-10-804-859-55

  Query Match            100.0%;  Score 20;  DB 8;  Length 60;
  Best Local Similarity  100.0%;  Pred. No. 6;
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Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db          7 CTTGCTCTGTTGCCCAGGCT 26


RESULT 3
US-10-467-851-277
; Sequence 277, Application US/10467851
; Publication No. US20050221303A1
; GENERAL INFORMATION:
;  APPLICANT: TELERMAN, Adam
;  APPLICANT:  AMSON, Robert
;  APPLICANT:  TUIJNDER, Marcel,
;  APPLICANT:  SUSINI, Laurent
;  TITLE OF INVENTION: SEQUENCES INVOLVED IN PHENOMENA OF TUMOUR SUPPRESSION,
;  TITLE OF INVENTION:  TUMOUR REVERSION, APOPTOSIS AND/OR VIRUS RESISTANCE
;  TITLE OF INVENTION:  AND THEIR USE AS MEDICINES
;  FILE REFERENCE: 11416-014-999
;  CURRENT APPLICATION NUMBER: US/10/467,851
;  CURRENT FILING DATE:  2003-08-13
;  PRIOR APPLICATION NUMBER: PCT/FR 02/00 543
;  PRIOR FILING DATE: 2002-02-13
;  PRIOR APPLICATION NUMBER: FR 01/01 925
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 1020
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 277
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-467-851-277

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  Best Local Similarity  100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         11 CTTGCTCTGTTGCCCAGGCT 30


RESULT 4
US-10-708-204-6674/c
; Sequence 6674, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6674
;   LENGTH: 72
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-6674

  Query Match            100.0%;  Score 20;  DB 9;  Length 72;
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Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         67 CTTGCTCTGTTGCCCAGGCT 48


RESULT 5
US-10-467-851-853/c
; Sequence 853, Application US/10467851
; Publication No. US20050221303A1
; GENERAL INFORMATION:
;  APPLICANT: TELERMAN, Adam
;  APPLICANT:  AMSON, Robert
;  APPLICANT:  TUIJNDER, Marcel,
;  APPLICANT:  SUSINI, Laurent
;  TITLE OF INVENTION: SEQUENCES INVOLVED IN PHENOMENA OF TUMOUR SUPPRESSION,
;  TITLE OF INVENTION:  TUMOUR REVERSION, APOPTOSIS AND/OR VIRUS RESISTANCE
;  TITLE OF INVENTION:  AND THEIR USE AS MEDICINES
;  FILE REFERENCE: 11416-014-999
;  CURRENT APPLICATION NUMBER: US/10/467,851
;  CURRENT FILING DATE:  2003-08-13
;  PRIOR APPLICATION NUMBER: PCT/FR 02/00 543
;  PRIOR FILING DATE: 2002-02-13
;  PRIOR APPLICATION NUMBER: FR 01/01 925
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 1020
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 853
;   LENGTH: 77
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-467-851-853

  Query Match            100.0%;  Score 20;  DB 9;  Length 77;
  Best Local Similarity  100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         39 CTTGCTCTGTTGCCCAGGCT 20


RESULT 6
US-10-708-204-6268/c
; Sequence 6268, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6268
;   LENGTH: 78
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-6268

  Query Match            100.0%;  Score 20;  DB 9;  Length 78;
  Best Local Similarity  100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
              ||||||||||||||||||||
Db         78 CTTGCTCTGTTGCCCAGGCT 59


RESULT 7
US-10-708-204-6998/c
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:59:57 ; Search time 246.08 Seconds
(without alignments)
65.779 Million cell updates/sec

Title: US-10-754-446-3
Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
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Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	20	100.0	21	6	US-10-310-914A-578793	Sequence 578793,
5	20	100.0	21	6	US-10-310-914A-611412	Sequence 611412,
6	20	100.0	21	6	US-10-310-914A-613165	Sequence 613165,
7	20	100.0	21	6	US-10-310-914A-762251	Sequence 762251,
8	20	100.0	21	6	US-10-310-914A-1015245	Sequence 1015245,
9	20	100.0	21	6	US-10-310-914A-1304732	Sequence 1304732,
10	20	100.0	21	6	US-10-310-914A-1312897	Sequence 1312897,
11	20	100.0	22	6	US-10-310-914A-156812	Sequence 156812,
12	20	100.0	22	6	US-10-310-914A-157391	Sequence 157391,
13	20	100.0	22	6	US-10-310-914A-184260	Sequence 184260,
14	20	100.0	22	6	US-10-310-914A-201989	Sequence 201989,
15	20	100.0	22	6	US-10-310-914A-228639	Sequence 228639,
16	20	100.0	22	6	US-10-310-914A-532105	Sequence 532105,
17	20	100.0	22	6	US-10-310-914A-611495	Sequence 611495,
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30	20	100.0	23	6	US-10-310-914A-212478	Sequence 212478,
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40	20	100.0	23	6	US-10-310-914A-572758	Sequence 572758,
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ALIGNMENTS

RESULT 1
US-10-310-914A-206955
; Sequence 206955, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 206955
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-206955

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Best Local Similarity 65.0%; Pred. No. 1.8;
Matches 13; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db          1 CUUGCUCUGUUGCCCAGGCU 20
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; Sequence 391931, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 21
; TYPE: RNA

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;   ORGANISM: Human
US-10-310-914A-391931

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  Matches   13;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
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Db          1 CUUGCUCUGUUGCCCAGGCU 20


RESULT 3
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; Sequence 437321, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
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;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-437321

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Qy          1 CTTGCTCTGTTGCCCAGGCT 20
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Db          1 CUUGCUCUGUUGCCCAGGCU 20


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US-10-310-914A-578793
; Sequence 578793, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 578793
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-578793

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  Best Local Similarity   65.0%;  Pred. No. 1.8;
  Matches   13;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
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; Sequence 611412, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 611412
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-611412

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  Best Local Similarity   65.0%;  Pred. No. 1.8;
  Matches   13;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 613165, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 613165
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-613165

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  Best Local Similarity   65.0%;  Pred. No. 1.8;
  Matches   13;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

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              |::||:|:|::||||||||:
Db          1 CUUGCUCUGUUGCCCAGGCU 20


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US-10-310-914A-762251
; Sequence 762251, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 762251
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
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GenCore version 5.1.6

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488.341 Million cell updates/sec

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Perfect score: 20
Sequence: 1 cttgctctgttgcccaggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	20	100.0	117	3	US-09-513-999C-17724	Sequence 17724, A
c	5	20	100.0	117	3	US-09-513-999C-24469	Sequence 24469, A
	6	20	100.0	128	3	US-09-513-999C-15044	Sequence 15044, A
c	7	20	100.0	145	3	US-09-621-976-14390	Sequence 14390, A
	8	20	100.0	145	3	US-09-513-999C-16178	Sequence 16178, A
	9	20	100.0	145	3	US-09-513-999C-25910	Sequence 25910, A
	10	20	100.0	151	3	US-09-513-999C-24127	Sequence 24127, A
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c	13	20	100.0	155	3	US-09-513-999C-29581	Sequence 29581, A
c	14	20	100.0	158	3	US-09-621-976-11688	Sequence 11688, A
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c	18	20	100.0	170	3	US-09-621-976-11644	Sequence 11644, A
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c	22	20	100.0	170	3	US-09-621-976-12076	Sequence 12076, A
c	23	20	100.0	170	3	US-09-621-976-12098	Sequence 12098, A
c	24	20	100.0	170	3	US-09-621-976-12260	Sequence 12260, A
c	25	20	100.0	170	3	US-09-621-976-12300	Sequence 12300, A
c	26	20	100.0	170	3	US-09-621-976-12391	Sequence 12391, A
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c	29	20	100.0	170	3	US-09-621-976-13550	Sequence 13550, A
c	30	20	100.0	171	3	US-09-621-976-11724	Sequence 11724, A
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c	44	20	100.0	173	3	US-09-621-976-12010	Sequence 12010, A
c	45	20	100.0	173	3	US-09-621-976-12151	Sequence 12151, A

ALIGNMENTS

RESULT 1
US-09-513-999C-20008/c
; Sequence 20008, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20008
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20008

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Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-513-999C-17342
; Sequence 17342, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26

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;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 17342
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-17342

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  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTGCTCTGTTGCCCAGGCT 20
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Db         78 CTTGCTCTGTTGCCCAGGCT 97


RESULT 3
US-09-513-999C-25323/c
; Sequence 25323, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 25323
;   LENGTH: 114
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-25323

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         91 CTTGCTCTGTTGCCCAGGCT 72


RESULT 4
US-09-513-999C-17724
; Sequence 17724, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 17724
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 9
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 11
;   OTHER INFORMATION: k=g or t
US-09-513-999C-17724

  Query Match            100.0%;  Score 20;  DB 3;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 5
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; Sequence 24469, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 24469
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-24469

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Qy          1 CTTGCTCTGTTGCCCAGGCT 20
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Db        112 CTTGCTCTGTTGCCCAGGCT 93


RESULT 6
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; Sequence 15044, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION: .
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 15044
;   LENGTH: 128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-15044

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GenCore version 5.1.6

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Perfect score: 22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	22	100.0	790	8	AF305572S3	AF305574 Homo sapi
c 2	22	100.0	1740	6	AX280021	AX280021 Sequence
c 3	22	100.0	1829	6	CQ719994	CQ719994 Sequence
c 4	22	100.0	2004	8	AF249319	AF249319 Homo sapi
c 5	22	100.0	2037	8	HSA293970	AJ293970 Homo sapi
c 6	22	100.0	2049	8	AK026102	AK026102 Homo sapi
c 7	22	100.0	2051	8	AF287269	AF287269 Homo sapi
c 8	22	100.0	2052	6	AX083508	AX083508 Sequence
c 9	22	100.0	2063	8	AK222673	AK222673 Homo sapi
c 10	22	100.0	2078	8	BC005149	BC005149 Homo sapi
c 11	22	100.0	2094	6	BD233734	BD233734 31 human
c 12	22	100.0	2095	6	AX280019	AX280019 Sequence
c 13	22	100.0	2272	8	HSA293659	AJ293659 Homo sapi
c 14	22	100.0	13270	8	AF287270	AF287270 Homo sapi
15	22	100.0	155645	14	AC021153	AC021153 Homo sapi
c 16	22	100.0	173126	8	AC008878	AC008878 Homo sapi
c 17	20.4	92.7	2065	8	AB125179	AB125179 Macaca fa
c 18	20	90.9	110000	1	AE014295_10	Continuation (11 o
c 19	20	90.9	349980	6	AX492785	AX492785 Sequence
c 20	20	90.9	349980	6	AX553952	AX553952 Sequence
c 21	17.8	80.9	717	10	BV552653	BV552653 S221P6043
22	17.8	80.9	734	10	BV539631	BV539631 G591P6424
23	17.8	80.9	767	10	BV534108	BV534108 G591P6224
24	17.8	80.9	775	10	BV539839	BV539839 G591P6408
25	17.8	80.9	826	10	BV532664	BV532664 G591P6209
26	17.8	80.9	1347	13	DQ103713	DQ103713 Influenza
c 27	17.8	80.9	3666	1	AB050784	AB050784 Sphingomo
c 28	17.8	80.9	7722	1	AB032203	AB032203 Sphingomo
29	17.8	80.9	24756	14	AC010403	AC010403 Homo sapi
30	17.8	80.9	69678	8	AC091573	AC091573 Homo sapi
31	17.8	80.9	143803	5	BX470131	BX470131 Zebrafish
c 32	17.8	80.9	157076	8	AC019031	AC019031 Homo sapi
c 33	17.8	80.9	174578	8	AC013287	AC013287 Homo sapi
34	17.8	80.9	177301	8	AC078868	AC078868 Homo sapi
c 35	17.8	80.9	182182	5	BX890617	BX890617 Zebrafish
36	17.8	80.9	212671	14	AC084849	AC084849 Homo sapi
37	17.8	80.9	213611	8	AF276759	AF276759 Homo sapi
c 38	17.8	80.9	242704	8	BS000230	BS000230 Pan trogl
39	17.4	79.1	3153	6	E15417	E15417 Arthrobacte
c 40	17.4	79.1	3700	1	STHISX	V01373 Salmonella
c 41	17.4	79.1	4483	1	STYHISTO	J01805 S. typhimur
42	17.4	79.1	8516	1	D88362	D88362 Arthrobacte
43	17.4	79.1	20518	1	AE008805	AE008805 Salmonell
44	17.4	79.1	40699	2	CEZK637	Z11115 Caenorhabdi
c 45	17.4	79.1	82568	15	AP004906	AP004906 Lotus cor

ALIGNMENTS

RESULT 1
AF305572S3/c
LOCUS AF305572S3 790 bp DNA linear PRI 26-DEC-2000
DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 3 and 4.
ACCESSION AF305574
VERSION AF305574.1 GI:11991200
KEYWORDS .
SEGMENT 3 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
PUBMED 10973263
REFERENCE 2 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES Location/Qualifiers
source 1. .790
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exon 267. .434
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exon 589. .757
/gene="MCOLN1"
/number=4
ORIGIN

Query Match 100.0%; Score 22; DB 8; Length 790;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TAACCACCATCGGATCAATGTC 22
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Db        750 TAACCACCATCGGATCAATGTC 729


RESULT 2
AX280021/c
LOCUS       AX280021               1740 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 3 from Patent WO0177331.
ACCESSION   AX280021
VERSION     AX280021.1  GI:16607475
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Curtis,R.A. and Silos-Santiago,I.
  TITLE     Human trp-like calcium channel protein-2 (tlcc-2)
  JOURNAL   Patent: WO 0177331-A 3 18-OCT-2001;
            MILLENIUM PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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     CDS             1. .>1740
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ORIGIN

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Qy          1 TAACCACCATCGGATCAATGTC 22
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Db        568 TAACCACCATCGGATCAATGTC 547


RESULT 3
CQ719994/c
LOCUS       CQ719994               1829 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 5928 from Patent WO02068579.
ACCESSION   CQ719994
VERSION     CQ719994.1  GI:42280851
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 5928 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 1829;
  Best Local Similarity   100.0%;  Pred. No. 0.96;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGTC 22
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Db        537 TAACCACCATCGGATCAATGTC 516


RESULT 4
AF249319/c
LOCUS       AF249319               2004 bp    mRNA    linear   PRI 22-SEP-2000
DEFINITION  Homo sapiens mucolipidosis type IV protein (MLIV) mRNA, complete
            cds.
ACCESSION   AF249319
VERSION     AF249319.1  GI:9971787
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2004)
  AUTHORS   Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
            Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
  TITLE     Identification of the gene causing mucolipidosis type IV
  JOURNAL   Nat. Genet. 26 (1), 118-123 (2000)
   PUBMED   10973263
REFERENCE   2  (bases 1 to 2004)
  AUTHORS   Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
            Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2000) Molecular Genetics, The Weizmann Institute
            of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES             Location/Qualifiers
     source          1. .2004
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .2004
                     /gene="MLIV"
     CDS             85. .1827
                     /gene="MLIV"
                     /note="causes mucolipidosis type IV"
                     /codon_start=1
                     /product="mucolipidosis type IV protein"
                     /protein_id="AAG10422.1"
                     /db_xref="GI:9971788"
                     /translation="MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPEEEDLRRR
                     LKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFR
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                     WRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT
                     STLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPY
                     HVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYM
                     VLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
                     CGRDPSEEHSLLVN"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 8;  Length 2004;
  Best Local Similarity   100.0%;  Pred. No. 0.97;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 2460.3 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-2
Perfect score: 22
Sequence: 1 taaccaccatcggatcaatgtc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	22	100.0	423	1	AW969529	AW969529 EST381606
c 2	22	100.0	425	3	BP391004	BP391004 BP391004
c 3	22	100.0	439	8	T66341	T66341 yc78b06.r1
4	22	100.0	480	1	AW328429	AW328429 ds02e06.x
c 5	22	100.0	510	2	BG272754	BG272754 nah89c03.
c 6	22	100.0	554	3	BP265945	BP265945 BP265945
c 7	22	100.0	580	3	BP266237	BP266237 BP266237
c 8	22	100.0	581	3	BP332355	BP332355 BP332355
c 9	22	100.0	657	3	BI819028	BI819028 603033154
c 10	22	100.0	660	3	BI836168	BI836168 603085896
c 11	22	100.0	660	3	BI907877	BI907877 603066872
c 12	22	100.0	663	3	BI523736	BI523736 603052025
c 13	22	100.0	663	3	BI836493	BI836493 603082706
c 14	22	100.0	666	3	BM005772	BM005772 603613386
c 15	22	100.0	666	6	CA391526	CA391526 cs16c04.y
c 16	22	100.0	672	3	BI490022	BI490022 603031806
c 17	22	100.0	678	8	DR001457	DR001457 TC113094
c 18	22	100.0	683	6	CF132757	CF132757 UI-HF-FQ0
c 19	22	100.0	696	2	BF529860	BF529860 602042214
c 20	22	100.0	697	3	BM049487	BM049487 603623420
c 21	22	100.0	705	3	BI822028	BI822028 603040071
c 22	22	100.0	709	3	BI825945	BI825945 603076515
c 23	22	100.0	743	3	BI771045	BI771045 603055394
c 24	22	100.0	790	6	CB988285	CB988285 AGENCOURT
c 25	22	100.0	810	3	BI753742	BI753742 603028260
c 26	22	100.0	818	2	BG831705	BG831705 602765791
c 27	22	100.0	846	5	BX383671	BX383671 BX383671
c 28	22	100.0	873	6	CD558014	CD558014 AGENCOURT
c 29	22	100.0	890	5	BX399044	BX399044 BX399044
c 30	22	100.0	901	5	BU542887	BU542887 AGENCOURT
c 31	22	100.0	902	5	BQ901107	BQ901107 AGENCOURT
c 32	22	100.0	909	5	BU543879	BU543879 AGENCOURT
c 33	22	100.0	910	5	BU552585	BU552585 AGENCOURT
c 34	22	100.0	962	5	BX402300	BX402300 BX402300
c 35	22	100.0	998	3	BI824195	BI824195 603040561
c 36	22	100.0	998	3	BM905707	BM905707 AGENCOURT
c 37	22	100.0	1026	5	BX364018	BX364018 BX364018
c 38	22	100.0	1047	2	BE795087	BE795087 601592613
c 39	22	100.0	1050	5	BX462609	BX462609 BX462609
c 40	22	100.0	1078	5	BX362786	BX362786 BX362786
c 41	22	100.0	1144	5	BX386808	BX386808 BX386808
c 42	22	100.0	1743	10	AY410283	AY410283 Homo sapi
c 43	22	100.0	1996	4	CR622331	CR622331 full-leng
c 44	20.4	92.7	951	5	BU195645	BU195645 AGENCOURT
c 45	20	90.9	540	3	BI516259	BI516259 BB160021B

ALIGNMENTS

RESULT 1
AW969529/c
LOCUS AW969529 423 bp mRNA linear EST 01-JUN-2000
DEFINITION EST381606 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
ACCESSION AW969529
VERSION AW969529.1 GI:8159373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 266
Seq primer: Forward.
FEATURES Location/Qualifiers
source 1. .423
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptSKm"
ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TAACCACCATCGGATCAATGTC 22
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Db         96 TAACCACCATCGGATCAATGTC 75
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RESULT 2
BP391004/c
LOCUS       BP391004                425 bp    mRNA    linear   EST 01-FEB-2005
DEFINITION  BP391004 Homo sapiens pancreatic islet Homo sapiens cDNA clone
            h-t-232-79 3', mRNA sequence.
ACCESSION   BP391004
VERSION     BP391004.1  GI:58414498
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Takeda,J., Jin,L. and Horikawa,Y.
  TITLE     Expression profile of mRNAs from human pancreatic islet tumors
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yukio Horikawa
            Laboratory of Molecular Genetics
            Institute for Molecular and Cellular Regulation, Gunma University
            Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan
            Tel: 81-27-220-8832
            Fax: 81-27-220-8889
            Email: yhorikaw@showa.gunma-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .425
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ORIGIN

  Query Match             100.0%;  Score 22;  DB 3;  Length 425;
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Qy          1 TAACCACCATCGGATCAATGTC 22
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Db         73 TAACCACCATCGGATCAATGTC 52


RESULT 3
T66341/c
LOCUS       T66341                  439 bp    mRNA    linear   EST 07-MAR-1995
DEFINITION  yc78b06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:21977 5', mRNA sequence.
ACCESSION   T66341
VERSION     T66341.1  GI:675386
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2264
            High qality sequence stops: 345 Source: IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
            Insert Length: 2264   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /sex="female"
                     /dev_stage="73 days post natal"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares infant brain 1NIB"
                     /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                     I; Site_2: Hind III; 1st strand cDNA was primed with a Not
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                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to Hind III adaptors
                     (Pharmacia), digested with Not I and directionally cloned
                     into the Not I and Hind III sites of the Lafmid BA vector.
                     Library went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 22;  DB 8;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGTC 22
              ||||||||||||||||||||||
Db        309 TAACCACCATCGGATCAATGTC 288


RESULT 4
AW328429
LOCUS       AW328429                480 bp    mRNA    linear   EST 28-JAN-2000
DEFINITION  ds02e06.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847443 5', mRNA
            sequence.
ACCESSION   AW328429
VERSION     AW328429.1  GI:6798925
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Edge BioSystems
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Plate: LLCM0030  row: I  column: 12
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
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                     /cell_line="MGC1"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_4"
                     /note="Organ: Cervix; Vector: pOTB7a; Site_1: SceI;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 298.496 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-2
Perfect score: 22
Sequence: 1 taaccaccatcggatcaatgtc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
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8: geneseqn2003as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	22	100.0	22	14	AEB28958	Aeb28958 Human MCO
	2	22	100.0	1619	4	AAI61022	Aai61022 Human pol
c	3	22	100.0	1740	6	AAI71700	Aai71700 Human TRP
c	4	22	100.0	1740	6	ABL40755	Abl40755 Human TLC
c	5	22	100.0	1741	4	AAI59236	Aai59236 Human pol
c	6	22	100.0	1743	9	ADB84284	Adb84284 Human muc
c	7	22	100.0	1743	14	ADV66231	Adv66231 TRP-like
c	8	22	100.0	2051	13	ADP25150	Adp25150 PRO polyp
c	9	22	100.0	2052	4	AAF81753	Aaf81753 Human mem
c	10	22	100.0	2092	5	AAS72274	Aas72274 DNA encod
c	11	22	100.0	2092	6	ABL90358	Abl90358 Human pol
c	12	22	100.0	2094	3	AAA39067	Aaa39067 Human sec
c	13	22	100.0	2095	6	AAI71699	Aai71699 Human TRP
c	14	22	100.0	2095	6	ABL40754	Abl40754 Human TLC
c	15	22	100.0	2095	14	ADV66229	Adv66229 TRP-like
c	16	22	100.0	2140	12	ADQ24925	Adq24925 Human sof
c	17	22	100.0	11365	4	AAK73827	Aak73827 Human imm
c	18	22	100.0	13270	9	ADB84283	Adb84283 Human muc
c	19	22	100.0	20046	4	AAK73826	Aak73826 Human imm
c	20	20	90.9	349980	6	ABQ81847	Abq81847 Bifidobac
c	21	18.4	83.6	2860	5	AAS65933	Aas65933 DNA encod
c	22	17.4	79.1	682	8	ACA49409	Aca49409 Prokaryot
c	23	17.4	79.1	687	8	ACA51484	Aca51484 Prokaryot
	24	17.4	79.1	3153	2	AAV19895	Aav19895 Glucodext
c	25	17.2	78.2	963	13	ADT46459	Adt46459 Bacterial
	26	16.8	76.4	447	13	ADT43994	Adt43994 Bacterial
	27	16.8	76.4	705	3	AAZ50958	Aaz50958 Agrobacte
	28	16.8	76.4	2505	13	ADU01691	Adu01691 Novel hum
	29	16.4	74.5	1153	4	ABL16397	Abl16397 Drosophil
c	30	16.4	74.5	1274	5	AAS79165	Aas79165 DNA encod
c	31	16.4	74.5	3208	4	ABL16396	Abl16396 Drosophil
c	32	16.4	74.5	4106	4	ABL17062	Abl17062 Drosophil
	33	16.4	74.5	110000	11	ADM27081_07	Continuation (8 of
	34	16.2	73.6	230	14	ADY99718	Ady99718 T_reesei
c	35	16.2	73.6	531	12	ACH70153	Ach70153 Human gen
c	36	16.2	73.6	1035	4	AAD08299	Aad08299 Human sec
c	37	16.2	73.6	1228	11	ADW22430	Adw22430 Rat chole
c	38	16.2	73.6	1339	13	ADT16087	Adt16087 Plant cDN
c	39	16.2	73.6	1638	13	ADT46663	Adt46663 Bacterial
c	40	16.2	73.6	2442	4	ABL08173	Abl08173 Drosophil
c	41	16.2	73.6	2609	13	ADX34421	Adx34421 Plant ful
c	42	16.2	73.6	3825	11	ACL28924	Acl28924 Rice abio
c	43	16.2	73.6	4442	4	ABL08172	Abl08172 Drosophil
c	44	16.2	73.6	4816	10	ADE54538	Ade54538 Rat gene
c	45	16.2	73.6	4816	10	ADE54542	Ade54542 Rat gene

ALIGNMENTS

RESULT 1
AEB28958
ID AEB28958 standard; DNA; 22 BP.
XX
AC AEB28958;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene PCR primer IVS-R SEQ ID NO:2.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 1; SEQ ID NO 2; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a PCR primer for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 22 BP; 7 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAACCACCATCGGATCAATGTC 22
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Db 1 TAACCACCATCGGATCAATGTC 22

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ID AAI61022 standard; cDNA; 1619 BP.
XX
AC AAI61022;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 5011.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM41866.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1; SEQ ID NO 5011; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1619 BP; 350 A; 450 C; 518 G; 301 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAACCACCATCGGATCAATGTC 22
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Db 1382 TAACCACCATCGGATCAATGTC 1403

RESULT 3
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ID AAI71700 standard; cDNA; 1740 BP.
XX
AC AAI71700;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #2.
XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1740
FT /*tag= a
FT /product= "TLCC-2"
FT /partial
XX
PN WO200177331-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011442.
XX
PR 07-APR-2000; 2000US-00544797.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-010913/01.
DR P-PSDB; AAM51858.
XX
PT Novel isolated human transient receptor potential-like calcium channel
PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
PT pain disorder, and cancer.
XX
PS Claim 1; Fig 1; 148pp; English.
XX
CC The present invention relates to the protein and coding sequences of

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 531.344 Seconds
(without alignments)
342.389 Million cell updates/sec

Title: US-10-754-446-2
Perfect score: 22
Sequence: 1 taaccaccatcggatcaatgtc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	22	100.0	1740	3	US-09-828-466-3	Sequence 3, Appli
c	5	22	100.0	1740	5	US-10-103-458-3	Sequence 3, Appli
c	6	22	100.0	1743	8	US-10-782-695-6	Sequence 6, Appli
c	7	22	100.0	2051	3	US-09-851-494B-2	Sequence 2, Appli
c	8	22	100.0	2052	3	US-09-965-529-50	Sequence 50, Appl
c	9	22	100.0	2052	3	US-09-969-680A-50	Sequence 50, Appl
c	10	22	100.0	2052	10	US-11-048-692-50	Sequence 50, Appl
c	11	22	100.0	2092	6	US-10-264-237-920	Sequence 920, App
c	12	22	100.0	2092	9	US-10-450-763-8078	Sequence 8078, Ap
c	13	22	100.0	2094	3	US-09-820-893-26	Sequence 26, Appl
c	14	22	100.0	2094	7	US-10-607-565-26	Sequence 26, Appl
c	15	22	100.0	2095	3	US-09-828-466-1	Sequence 1, Appli
c	16	22	100.0	2095	5	US-10-103-458-1	Sequence 1, Appli
c	17	22	100.0	2095	8	US-10-782-695-4	Sequence 4, Appli
c	18	22	100.0	2140	8	US-10-723-860-7745	Sequence 7745, Ap
c	19	22	100.0	13270	3	US-09-851-494B-1	Sequence 1, Appli
c	20	20	90.9	25	10	US-11-060-756-171643	Sequence 171643,
c	21	20	90.9	2256646	7	US-10-470-565-1	Sequence 1, Appli
c	22	18.4	83.6	2860	9	US-10-450-763-1737	Sequence 1737, Ap
c	23	17.4	79.1	682	7	US-10-282-122A-37279	Sequence 37279, A
c	24	17.4	79.1	687	7	US-10-282-122A-39354	Sequence 39354, A
	25	17.2	78.2	496	7	US-10-424-599-142334	Sequence 142334,
c	26	17.2	78.2	963	6	US-10-369-493-44897	Sequence 44897, A
c	27	17.2	78.2	2731748	7	US-10-297-465A-1	Sequence 1, Appli
	28	16.8	76.4	447	6	US-10-369-493-42432	Sequence 42432, A
c	29	16.8	76.4	493	4	US-09-925-065A-364043	Sequence 364043,
c	30	16.8	76.4	24708	3	US-09-924-101-7	Sequence 7, Appli
c	31	16.4	74.5	25	9	US-10-843-527-25559	Sequence 25559, A
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	34	16.4	74.5	521	4	US-09-925-065A-636380	Sequence 636380,
	35	16.4	74.5	1153	10	US-11-097-143-21836	Sequence 21836, A
c	36	16.4	74.5	1274	9	US-10-450-763-14969	Sequence 14969, A
c	37	16.4	74.5	3208	10	US-11-097-143-21835	Sequence 21835, A
c	38	16.4	74.5	4106	10	US-11-097-143-22834	Sequence 22834, A
	39	16.2	73.6	230	9	US-10-950-009-1072	Sequence 1072, Ap
	40	16.2	73.6	506	4	US-09-925-065A-235084	Sequence 235084,
c	41	16.2	73.6	531	6	US-10-029-386-3348	Sequence 3348, Ap
c	42	16.2	73.6	554	4	US-09-925-065A-523439	Sequence 523439,
c	43	16.2	73.6	554	4	US-09-925-065A-523440	Sequence 523440,
	44	16.2	73.6	557	4	US-09-925-065A-940573	Sequence 940573,
	45	16.2	73.6	600	9	US-10-972-079-19463	Sequence 19463, A

ALIGNMENTS

RESULT 1
US-10-754-446-2
; Sequence 2, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-754-446-2

Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAACCACCATCGGATCAATGTC 22
||||||||||||||||||||||
Db 1 TAACCACCATCGGATCAATGTC 22

RESULT 2
US-11-060-756-2850/c
; Sequence 2850, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2850

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;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-2850

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  Best Local Similarity  100.0%;  Pred. No. 0.92;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         42 TAACCACCATCGGATCAATGTC 21


RESULT 3
US-11-060-756-7122/c
; Sequence 7122, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7122
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-7122

  Query Match            100.0%;  Score 22;  DB 10;  Length 1400;
  Best Local Similarity  100.0%;  Pred. No. 0.92;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGTC 22
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Db         42 TAACCACCATCGGATCAATGTC 21


RESULT 4
US-09-828-466-3/c
; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Immaculada
;  TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
;  FILE REFERENCE: MNI-125CP
;  CURRENT APPLICATION NUMBER: US/09/828,466
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 09/544,797
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1740
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1740)
US-09-828-466-3

  Query Match            100.0%;  Score 22;  DB 3;  Length 1740;
  Best Local Similarity  100.0%;  Pred. No. 0.94;
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Qy          1 TAACCACCATCGGATCAATGTC 22
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Db        568 TAACCACCATCGGATCAATGTC 547


RESULT 5
US-10-103-458-3/c
; Sequence 3, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
;  FILE REFERENCE: MNI-125
;  CURRENT APPLICATION NUMBER: US/10/103,458
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: US/09/544,797
;  PRIOR FILING DATE: PEIOE FILING DATE:  2000-04-07
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1740
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1740)
US-10-103-458-3

  Query Match            100.0%;  Score 22;  DB 5;  Length 1740;
  Best Local Similarity  100.0%;  Pred. No. 0.94;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGTC 22
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Db        568 TAACCACCATCGGATCAATGTC 547


RESULT 6
US-10-782-695-6/c
; Sequence 6, Application US/10782695
; Publication No. US20040248160A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria A.
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Tsai,  Fong-Ying
;  APPLICANT:  Hodge, Martin R.
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Bandaru, Rajasekhar
;  TITLE OF INVENTION: NOVEL 14275, 54420, 8797, 27439, 68730,
;  TITLE OF INVENTION:  69112 AND 52908 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI04-002OMNIM
;  CURRENT APPLICATION NUMBER: US/10/782,695
;  CURRENT FILING DATE:  2004-02-19
;  PRIOR APPLICATION NUMBER: US 09/945,254
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/229,829
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: US 09/945,301
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/229,301
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: US 10/007,399
;  PRIOR FILING DATE: 2001-11-05
;  PRIOR APPLICATION NUMBER: US 09/390,039
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: US 09/146,416
;  PRIOR FILING DATE: 1998-09-03
;  PRIOR APPLICATION NUMBER: US 10/024,036
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US 60/258,222
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 10/103,458
;  PRIOR FILING DATE: 2002-03-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:59:57 ; Search time 270.688 Seconds
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Perfect score: 22
Sequence: 1 taaccaccatcggatcaatgtc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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c	2	16.8	76.4	1107	6	US-10-750-623-53745	Sequence 53745, A
	3	16.2	73.6	1458	7	US-11-133-360-4	Sequence 4, Appli
	4	16.2	73.6	1786	6	US-10-750-185-46643	Sequence 46643, A
	5	16.2	73.6	1786	6	US-10-750-623-46643	Sequence 46643, A
	6	15.8	71.8	600	7	US-11-128-061-3932	Sequence 3932, Ap
	7	15.8	71.8	669	7	US-11-128-061-290	Sequence 290, App
	8	15.8	71.8	2081	6	US-10-750-185-27573	Sequence 27573, A
	9	15.8	71.8	2081	6	US-10-750-623-27573	Sequence 27573, A
	10	15.6	70.9	506	7	US-11-128-061-2800	Sequence 2800, Ap
	11	15.6	70.9	506	7	US-11-128-061-6442	Sequence 6442, Ap
c	12	15.6	70.9	98345	7	US-11-112-908-36	Sequence 36, Appl
c	13	15.6	70.9	127340	7	US-11-112-908-35	Sequence 35, Appl
c	14	15.6	70.9	157224	7	US-11-112-908-51	Sequence 51, Appl
c	15	15.6	70.9	170189	7	US-11-112-908-50	Sequence 50, Appl
c	16	15.4	70.0	88873	6	US-10-995-561-13383	Sequence 13383, A
c	17	15.4	70.0	146656	7	US-11-121-086-68	Sequence 68, Appl
	18	15.4	70.0	154452	7	US-11-121-086-74	Sequence 74, Appl
c	19	15.4	70.0	190882	7	US-11-121-086-69	Sequence 69, Appl
c	20	15.2	69.1	25	7	US-11-136-527-311442	Sequence 311442,
c	21	15.2	69.1	25	7	US-11-136-527-311448	Sequence 311448,
c	22	15.2	69.1	448	7	US-11-123-896-406	Sequence 406, App
c	23	15.2	69.1	600	7	US-11-136-527-6599	Sequence 6599, Ap
c	24	15.2	69.1	1870	6	US-10-750-185-38563	Sequence 38563, A
c	25	15.2	69.1	1870	6	US-10-750-623-38563	Sequence 38563, A
c	26	15.2	69.1	3328	7	US-11-136-527-2503	Sequence 2503, Ap
c	27	15	68.2	1400	7	US-11-136-527-4366	Sequence 4366, Ap
c	28	15	68.2	2746	7	US-11-136-527-270	Sequence 270, App
c	29	14.8	67.3	25	7	US-11-136-527-311434	Sequence 311434,
c	30	14.8	67.3	1509	6	US-10-454-437-211	Sequence 211, App
	31	14.8	67.3	4091	6	US-10-750-185-32344	Sequence 32344, A
	32	14.8	67.3	4091	6	US-10-750-623-32344	Sequence 32344, A
c	33	14.8	67.3	182303	7	US-11-121-086-45	Sequence 45, Appl
c	34	14.6	66.4	408	6	US-10-793-626-2675	Sequence 2675, Ap
c	35	14.6	66.4	600	6	US-10-750-185-3617	Sequence 3617, Ap
c	36	14.6	66.4	600	6	US-10-750-623-3617	Sequence 3617, Ap
c	37	14.6	66.4	1161	6	US-10-793-626-2299	Sequence 2299, Ap
	38	14.6	66.4	1398	7	US-11-133-360-2	Sequence 2, Appli
	39	14.6	66.4	1401	7	US-11-133-360-6	Sequence 6, Appli
	40	14.6	66.4	1401	7	US-11-133-360-8	Sequence 8, Appli
c	41	14.6	66.4	1951	6	US-10-750-185-64757	Sequence 64757, A
c	42	14.6	66.4	1951	6	US-10-750-623-64757	Sequence 64757, A
	43	14.6	66.4	2083	7	US-11-167-856-15	Sequence 15, Appl
	44	14.6	66.4	2290	6	US-10-750-185-44532	Sequence 44532, A
	45	14.6	66.4	2290	6	US-10-750-623-44532	Sequence 44532, A

ALIGNMENTS

RESULT 1
US-10-750-185-53745/c
; Sequence 53745, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53745
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Bovine 19866881030294
US-10-750-185-53745

Query Match 76.4%; Score 16.8; DB 6; Length 1107;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db        800 TAACCACCATCTGATCCATG 781
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US-10-750-623-53745/c
; Sequence 53745, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

```
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53745
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Bovine  19866881030294
US-10-750-623-53745

  Query Match            76.4%;  Score 16.8;  DB 6;  Length 1107;
  Best Local Similarity   90.0%;  Pred. No. 45;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db        800 TAACCACCATCTGATCCATG 781


RESULT 3
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; Sequence 4, Application US/11133360
; Publication No. US20050287172A1
; GENERAL INFORMATION:
;  APPLICANT: MedImmune Vaccines, Inc et al.
;  TITLE OF INVENTION: INFLUENZA HEMAGGLUTININ AND NEURAMINIDASE VARIANTS
;  FILE REFERENCE: FL260
;  CURRENT APPLICATION NUMBER: US/11/133,360
;  CURRENT FILING DATE:  2005-05-20
;  PRIOR APPLICATION NUMBER: 60/574,553
;  PRIOR FILING DATE: 2004-05-25
;  PRIOR APPLICATION NUMBER: 60/657,554
;  PRIOR FILING DATE: 2005-02-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 1458
;   TYPE: DNA
;   ORGANISM: Influenza virus
US-11-133-360-4

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Qy          1 TAACCACCATCGGATCAATGT 21
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Db         40 TAACAACCATTGGATCAATCT 60


RESULT 4
US-10-750-185-46643
; Sequence 46643, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 46643
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Bovine  19866881022693
US-10-750-185-46643

  Query Match            73.6%;  Score 16.2;  DB 6;  Length 1786;
  Best Local Similarity   85.7%;  Pred. No. 92;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGT 21
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Db        882 TGACCACCATCGCATCACTGT 902


RESULT 5
US-10-750-623-46643
; Sequence 46643, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 46643
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Bovine  19866881022693
US-10-750-623-46643

  Query Match            73.6%;  Score 16.2;  DB 6;  Length 1786;
  Best Local Similarity   85.7%;  Pred. No. 92;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGT 21
              | ||||||||||  |||| |||
Db        882 TGACCACCATCGCATCACTGT 902


RESULT 6
US-11-128-061-3932
; Sequence 3932, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
;  TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
;  FILE REFERENCE: 01997.027701
;  CURRENT APPLICATION NUMBER: US/11/128,061
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
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GenCore version 5.1.6

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Perfect score: 22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	22	100.0	15353	3	US-09-949-016-13454	Sequence 13454, A
c	3	16	72.7	1650	3	US-09-107-532A-3186	Sequence 3186, Ap
c	4	15.8	71.8	537	3	US-09-489-039A-5168	Sequence 5168, Ap
	5	15.8	71.8	572	3	US-09-533-559-6112	Sequence 6112, Ap
	6	15.8	71.8	601	3	US-09-949-016-79854	Sequence 79854, A
c	7	15.8	71.8	601	3	US-09-949-016-83923	Sequence 83923, A
	8	15.8	71.8	1614	2	US-08-867-941-10	Sequence 10, Appl
	9	15.8	71.8	1614	3	US-09-074-658-10	Sequence 10, Appl
	10	15.8	71.8	1623	2	US-08-867-941-5	Sequence 5, Appli
	11	15.8	71.8	1623	3	US-09-074-658-5	Sequence 5, Appli
	12	15.8	71.8	1635	3	US-09-540-236-840	Sequence 840, App
	13	15.8	71.8	4657	3	US-09-254-325-1	Sequence 1, Appli
	14	15.8	71.8	5643	3	US-09-079-415-5	Sequence 5, Appli
	15	15.8	71.8	5643	3	US-08-750-458A-1	Sequence 1, Appli
	16	15.8	71.8	7641	2	US-08-867-941-6	Sequence 6, Appli
	17	15.8	71.8	7641	3	US-09-074-658-6	Sequence 6, Appli
	18	15.8	71.8	7650	2	US-08-867-941-1	Sequence 1, Appli
	19	15.8	71.8	7650	3	US-09-074-658-1	Sequence 1, Appli
c	20	15.8	71.8	41322	3	US-10-024-396-13	Sequence 13, Appl
	21	15.8	71.8	49617	3	US-09-596-002-28	Sequence 28, Appl
c	22	15.8	71.8	90472	3	US-09-949-016-14038	Sequence 14038, A
	23	15.8	71.8	96340	3	US-09-949-016-15863	Sequence 15863, A
c	24	15.8	71.8	455726	3	US-09-949-016-14157	Sequence 14157, A
c	25	15.8	71.8	481115	3	US-09-949-016-11940	Sequence 11940, A
	26	15.6	70.9	762	3	US-09-252-991A-3481	Sequence 3481, Ap
c	27	15.6	70.9	816	3	US-09-489-039A-4176	Sequence 4176, Ap
c	28	15.6	70.9	834	3	US-09-489-039A-2174	Sequence 2174, Ap
c	29	15.6	70.9	1203	3	US-09-252-991A-3468	Sequence 3468, Ap
	30	15.6	70.9	1269	3	US-09-252-991A-3470	Sequence 3470, Ap
c	31	15.6	70.9	1428	3	US-09-248-796A-3428	Sequence 3428, Ap
c	32	15.6	70.9	1697	3	US-09-270-767-10255	Sequence 10255, A
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	35	15.6	70.9	2231	3	US-09-949-016-4932	Sequence 4932, Ap
	36	15.6	70.9	2231	3	US-09-949-016-4933	Sequence 4933, Ap
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c	38	15.6	70.9	4081	3	US-08-999-774A-1	Sequence 1, Appli
c	39	15.6	70.9	4558	2	US-08-309-512-2	Sequence 2, Appli
c	40	15.6	70.9	4558	6	PCT-US92-08756A-2	Sequence 2, Appli
c	41	15.6	70.9	7400	2	US-07-674-852-1	Sequence 1, Appli
c	42	15.6	70.9	7400	3	US-08-473-185-1	Sequence 1, Appli
c	43	15.6	70.9	7400	3	US-09-171-387-3	Sequence 3, Appli
	44	15.6	70.9	113379	3	US-09-949-016-17561	Sequence 17561, A
	45	15.6	70.9	113379	3	US-09-949-016-17562	Sequence 17562, A

ALIGNMENTS

RESULT 1
US-09-949-016-1712/c
; Sequence 1712, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1712
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1712

Query Match 100.0%; Score 22; DB 3; Length 2051;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TAACCACCATCGGATCAATGTC 22
              ||||||||||||||||||||||
Db        693 TAACCACCATCGGATCAATGTC 672
```

RESULT 2
US-09-949-016-13454/c
; Sequence 13454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13454
;   LENGTH: 15353
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13454

  Query Match            100.0%;  Score 22;  DB 3;  Length 15353;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAATGTC 22
              ||||||||||||||||||||||
Db       6298 TAACCACCATCGGATCAATGTC 6277


RESULT 3
US-09-107-532A-3186/c
; Sequence 3186, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3186:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1650 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...1650
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3186:
US-09-107-532A-3186

  Query Match            72.7%;  Score 16;  DB 3;  Length 1650;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AACCACCATCGGATCA 17
              ||||||||||||||||
Db        578 AACCACCATCGGATCA 563


RESULT 4
US-09-489-039A-5168/c
; Sequence 5168, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 5168
;   LENGTH: 537
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5168

  Query Match            71.8%;  Score 15.8;  DB 3;  Length 537;
  Best Local Similarity   89.5%;  Pred. No. 2.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TAACCACCATCGGATCAAT 19
              |||||||||| | |||||
Db        151 TAACCACCATCAGTTCAAT 133


RESULT 5
US-09-533-559-6112
; Sequence 6112, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
;  APPLICANT: Randy M. Berka
;  APPLICANT: Michael W. Rey
;  APPLICANT: Jeffrey R.Shuster
;  APPLICANT: Sakari Kauppinen
;  APPLICANT: Ib Groth Clausen
;  APPLICANT: Peter Bjarke Olsen
;  TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;  TITLE OF INVENTION: Expression
;  FILE REFERENCE: 5849.200-US
;  CURRENT APPLICATION NUMBER: US/09/533,559
;  CURRENT FILING DATE: 2000-03-22
;  EARLIER APPLICATION NUMBER: 09/273,623
;  EARLIER FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 7860
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6112
;   LENGTH: 572
;   TYPE: DNA
;   ORGANISM: Aspergillus oryzae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(572)
;   OTHER INFORMATION: n = A,T,C or G
US-09-533-559-6112

  Query Match            71.8%;  Score 15.8;  DB 3;  Length 572;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:49:05 ; Search time 736.68 Seconds
(without alignments)
1157.425 Million cell updates/sec

Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	790	8	AF305572S3	AF305574 Homo sapi
2		15	100.0	13270	8	AF287270	AF287270 Homo sapi
3	c	15	100.0	21081	2	AF106590	AF106590 Caenorhab
4	c	15	100.0	36859	2	AF003141	AF003141 Caenorhab
5		15	100.0	103303	14	AY339213	AY339213 Takifugu
6		15	100.0	110000	1	AE017180_03	Continuation (4 of
7	c	15	100.0	155645	14	AC021153	AC021153 Homo sapi
8	c	15	100.0	166981	14	AC157751	AC157751 Callithri
9		15	100.0	173126	8	AC008878	AC008878 Homo sapi
10		15	100.0	180213	14	AC150812	AC150812 Callithri
11	c	15	100.0	197202	14	AC153077	AC153077 Callithri
12		15	100.0	208232	9	AC149085	AC149085 Mus muscu
13		15	100.0	221553	9	AC149282	AC149282 Mus muscu
14		15	100.0	228698	14	AC127479	AC127479 Mus muscu
15	c	15	100.0	237653	14	AC073760	AC073760 Mus muscu
16		15	100.0	291000	1	SCO939105	AL939105 Streptomy
17	c	14	93.3	563	15	AJ836913	AJ836913 Arabidops
18		14	93.3	789	9	AF296282	AF296282 Mus muscu
19		14	93.3	789	9	AF296283	AF296283 Mus muscu
20	c	14	93.3	1250	9	S70756S1	S70756 Tlx-1=homeo
21	c	14	93.3	1950	6	AR622581	AR622581 Sequence
22		14	93.3	2262	9	AB127583	AB127583 Mus muscu
23		14	93.3	2428	8	AK096823	AK096823 Homo sapi
24	c	14	93.3	2685	9	BC059941	BC059941 Mus muscu
25	c	14	93.3	3238	5	AF427524	AF427524 Danio rer
26	c	14	93.3	4102	6	CQ986467	CQ986467 Sequence
27	c	14	93.3	10246	9	MMU251787	AJ251787 Mus muscu
28	c	14	93.3	10586	1	AE004991	AE004991 Halobacte
29	c	14	93.3	10696	1	AE012476	AE012476 Xanthomon
30	c	14	93.3	20074	8	HSA9794	AJ009794 Homo sapi
31	c	14	93.3	20232	6	AR619802	AR619802 Sequence
32		14	93.3	45653	5	BX323016	BX323016 Zebrafish
33	c	14	93.3	51099	8	AL357395	AL357395 Human DNA
34	c	14	93.3	53425	14	AY211534	AY211534 Zea mays
35	c	14	93.3	89015	14	AC008458	AC008458 Homo sapi
36	c	14	93.3	94092	14	AC155398	AC155398 Zea mays
37	c	14	93.3	110000	1	AE016822_15	Continuation (16 o
38	c	14	93.3	110000	1	AE017282_18	Continuation (19 o
39	c	14	93.3	110000	1	AE017282_29	Continuation (30 o
40	c	14	93.3	110000	1	AE017340_16	Continuation (17 o
41		14	93.3	110000	1	AP006618_44	Continuation (45 o
42		14	93.3	110000	1	AP006618_45	Continuation (46 o
43	c	14	93.3	110000	1	AP006618_58	Continuation (59 o
44		14	93.3	110000	1	AY596297_08	Continuation (9 of
45		14	93.3	110000	1	AY596297_28	Continuation (29 o

ALIGNMENTS

RESULT 1
AF305572S3
LOCUS AF305572S3 790 bp DNA linear PRI 26-DEC-2000
DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 3 and 4.
ACCESSION AF305574
VERSION AF305574.1 GI:11991200
KEYWORDS .
SEGMENT 3 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
PUBMED 10973263
REFERENCE 2 (bases 1 to 790)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES Location/Qualifiers
source 1. .790
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
exon 267. .434
/gene="MCOLN1"
/number=3
exon 589. .757
/gene="MCOLN1"
/number=4
ORIGIN

Query Match 100.0%; Score 15; DB 8; Length 790;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCGGGCCGGACTCA 15
              ||||||||||||||||
Db        548 AGCGGGCCGGACTCA 562


RESULT 2
AF287270
LOCUS       AF287270               13270 bp    DNA     linear   PRI 30-OCT-2000
DEFINITION  Homo sapiens mucolipin (MCOLN1) gene, complete cds.
ACCESSION   AF287270
VERSION     AF287270.1  GI:9844925
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 13270)
  AUTHORS   Sun,M., Goldin,E., Stahl,S., Falardeau,J.L., Kennedy,J.C.,
            Acierno,J.S. Jr., Bove,C., Kaneski,C.R., Nagle,J., Bromley,M.C.,
            Colman,M., Schiffmann,R. and Slaugenhaupt,S.A.
  TITLE     Mucolipidosis type IV is caused by mutations in a gene encoding a
            novel transient receptor potential channel
  JOURNAL   Hum. Mol. Genet. 9 (17), 2471-2478 (2000)
   PUBMED   11030752
REFERENCE   2  (bases 1 to 13270)
  AUTHORS   Slaugenhaupt,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institute
            of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
            Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .13270
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.3"
     gene            1401. .12753
                     /gene="MCOLN1"
     mRNA            join(1401. .1556,3736. .3941,5214. .5381,5536. .5701,
                     6295. .6403,6639. .6735,6933. .7032,7372. .7478,7596. .7745,
                     7876. .7977,8365. .8487,9061. .9276,12298. .12428,
                     12534. .12753)
                     /gene="MCOLN1"
                     /product="mucolipin"
     CDS             join(1526. .1556,3736. .3941,5214. .5381,5536. .5701,
                     6295. .6403,6639. .6735,6933. .7032,7372. .7478,7596. .7745,
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                     12534. .12570)
                     /gene="MCOLN1"
                     /codon_start=1
                     /product="mucolipin"
                     /protein_id="AAG00798.1"
                     /db_xref="GI:9844926"
                     /translation="MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPEEEDLRRR
                     LKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFR
                     HLFLLGYSDGADDTFAAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGDPWTNG
                     SGLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPPSDDLTLLESSSSY
                     KNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLE
                     TQAHIQECKHPSVFQHGDNSFRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFM
                     WRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT
                     STLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPY
                     HVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYM
                     VLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
                     CGRDPSEEHSLLVN"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 8;  Length 13270;
  Best Local Similarity  100.0%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCGGGCCGGACTCA 15
              ||||||||||||||||
Db       5495 AGCGGGCCGGACTCA 5509


RESULT 3
AF106590/c
LOCUS       AF106590               21081 bp    DNA     linear   INV 21-SEP-2004
DEFINITION  Caenorhabditis elegans cosmid F08B6, complete sequence.
ACCESSION   AF106590
VERSION     AF106590.1  GI:3886091
KEYWORDS    HTG.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 21081)
  AUTHORS   .
  CONSRTM   WormBase Consortium
  TITLE     Genome sequence of the nematode C. elegans: a platform for
            investigating biology. The C. elegans Sequencing Consortium
  JOURNAL   Science 282 (5396), 2012-2018 (1998)
   PUBMED   9851916
REFERENCE   2  (bases 1 to 21081)
  AUTHORS   Le,T.T., Scheet,P. and Kemp,K.
  TITLE     The sequence of C. elegans cosmid F08B6
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   4  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   5  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   6  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   7  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   8  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAY-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   9  (bases 1 to 21081)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-NOV-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   10 (bases 1 to 21081)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-2003) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:55:50 ; Search time 1677.48 Seconds
(without alignments)
418.369 Million cell updates/sec

Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	100.0	301	5	BY345580	BY345580 BY345580
c	2	15	100.0	331	5	BY345176	BY345176 BY345176
c	3	15	100.0	338	5	BY102360	BY102360 BY102360
c	4	15	100.0	375	5	BY087147	BY087147 BY087147
	5	15	100.0	375	5	C08554	C08554 C08554 Yuji
c	6	15	100.0	378	5	BY299457	BY299457 BY299457
	7	15	100.0	379	5	C71190	C71190 C71190 Yuji
	8	15	100.0	387	9	CC423137	CC423137 PUEHT72TD
	9	15	100.0	469	1	AV631303	AV631303 AV631303
c	10	15	100.0	480	5	BY249487	BY249487 BY249487
	11	15	100.0	502	7	CK583489	CK583489 IST_WI5_4
	12	15	100.0	519	7	CK583423	CK583423 IST_WI5_4
	13	15	100.0	568	7	CK577649	CK577649 IST_WI5_1
	14	15	100.0	624	3	BI726669	BI726669 1031086F1
	15	15	100.0	638	1	AU200865	AU200865 AU200865
	16	15	100.0	779	10	CG116594	CG116594 PUIED41TB
	17	15	100.0	786	10	AG602966	AG602966 Mus muscu
	18	15	100.0	797	7	CN200405	CN200405 Tor10084
	19	15	100.0	832	8	CX892033	CX892033 JGI_CAAM4
c	20	15	100.0	962	6	CA464646	CA464646 AGENCOURT
c	21	15	100.0	1040	3	BQ278046	BQ278046 AGENCOURT
c	22	14	93.3	194	3	BQ082114	BQ082114 K-EST0057
	23	14	93.3	208	2	BB568361	BB568361 BB568361
	24	14	93.3	287	9	AZ121792	AZ121792 RPCI-23-4
c	25	14	93.3	301	1	AI029662	AI029662 UI-R-C0-j
	26	14	93.3	306	2	BE419855	BE419855 WWS018.C1
	27	14	93.3	350	8	W66660	W66660 me23f09.r1
c	28	14	93.3	354	5	BY312288	BY312288 BY312288
	29	14	93.3	356	8	W99177	W99177 mf91h01.r1
	30	14	93.3	360	5	C45921	C45921 C45921 Yuji
	31	14	93.3	374	5	C43796	C43796 C43796 Yuji
c	32	14	93.3	389	8	DN368435	DN368435 LIB3731-0
	33	14	93.3	402	11	DR18I14S	AL738904 Danio rer
c	34	14	93.3	409	5	BY237451	BY237451 BY237451
	35	14	93.3	436	9	AZ251529	AZ251529 RPCI-23-4
	36	14	93.3	455	1	AA050210	AA050210 mj17b11.r
	37	14	93.3	462	5	BX527893	BX527893 BX527893
c	38	14	93.3	469	7	CJ034986	CJ034986 CJ034986
	39	14	93.3	471	8	W99993	W99993 mg27d06.r1
c	40	14	93.3	473	8	DN367700	DN367700 LIB3731-0
c	41	14	93.3	484	5	BX635951	BX635951 BX635951
c	42	14	93.3	487	10	CG732852	CG732852 1119151F1
	43	14	93.3	489	8	DN481676	DN481676 tef7_n20.
	44	14	93.3	489	10	CG465566	CG465566 KRIBB_2D_
c	45	14	93.3	491	2	BE943858	BE943858 UI-M-BH3-

ALIGNMENTS

RESULT 1
BY345580/c
LOCUS BY345580 301 bp mRNA linear EST 12-DEC-2002
DEFINITION BY345580 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L730015A09 5', mRNA sequence.
ACCESSION BY345580
VERSION BY345580.1 GI:26575068
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .301
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L730015A09"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"

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Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCGGGCCGGACTCA 15
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Db 17 AGCGGGCCGGACTCA 3

RESULT 2
BY345176/c
LOCUS BY345176 331 bp mRNA linear EST 12-DEC-2002
DEFINITION BY345176 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L730012A07 5', mRNA sequence.
ACCESSION BY345176
VERSION BY345176.1 GI:26574664
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 331)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
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COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .331
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L730012A07"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"

ORIGIN

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:15:14 ; Search time 203.52 Seconds
(without alignments)
491.207 Million cell updates/sec

Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	14	AEB28957	Aeb28957 Human MCO
	2	15	100.0	11365	4	AAK73827	Aak73827 Human imm
	3	15	100.0	13270	9	ADB84283	Adb84283 Human muc
	4	15	100.0	20046	4	AAK73826	Aak73826 Human imm
	5	14	93.3	318	6	ABQ91193	Abq91193 M. capsul
	6	14	93.3	432	12	ADL84655	Adl84655 DNA up-re
	7	14	93.3	432	12	ADL84656	Adl84656 DNA up-re
c	8	14	93.3	837	13	ADS61839	Ads61839 Bacterial
c	9	14	93.3	1950	14	ACL67519	Acl67519 M. xanthu
	10	14	93.3	2378	4	AAH23696	Aah23696 Human tum
c	11	14	93.3	4102	14	ADW10212	Adw10212 Colon pro
c	12	14	93.3	20232	14	ACL64734	Acl64734 M. xanthu
	13	14	93.3	28906	4	AAH23705	Aah23705 Human tum
	14	13.4	89.3	97	3	AAC17228	Aac17228 Human sec
c	15	13.4	89.3	163	2	AAQ75814	Aaq75814 AAV ITR.
	16	13.4	89.3	252	12	ACH93047	Ach93047 Human gen
	17	13.4	89.3	303	6	ABK78538	Abk78538 Bacillus
	18	13.4	89.3	365	3	AAA43414	Aaa43414 Rat secre
c	19	13.4	89.3	399	5	AAF66900	Aaf66900 Novel hum
	20	13.4	89.3	429	4	AAK60192	Aak60192 Human imm
	21	13.4	89.3	471	6	ABQ90279	Abq90279 M. capsul
	22	13.4	89.3	541	12	ADP81041	Adp81041 Human ova
	23	13.4	89.3	556	12	ACH79347	Ach79347 Human gen
c	24	13.4	89.3	616	3	AAF08076	Aaf08076 Fusarium
c	25	13.4	89.3	616	13	ADU52117	Adu52117 Fusarium
c	26	13.4	89.3	616	14	ADZ90120	Adz90120 Fusarium
	27	13.4	89.3	648	13	ADS63824	Ads63824 Bacterial
	28	13.4	89.3	648	13	ADS64203	Ads64203 Bacterial
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	30	13.4	89.3	681	9	ACD10983	Acd10983 Human col
	31	13.4	89.3	832	12	ADP81042	Adp81042 Human ova
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	34	13.4	89.3	968	3	AAF15010	Aaf15010 Trichoder
	35	13.4	89.3	968	13	ADU59051	Adu59051 Trichoder
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c	37	13.4	89.3	981	11	ACH94304	Ach94304 Klebsiell
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	42	13.4	89.3	1626	13	ADS59288	Ads59288 Bacterial
	43	13.4	89.3	1676	14	ADY17906	Ady17906 DNA encod
	44	13.4	89.3	1785	12	ADO07773	Ado07773 Mouse pol
	45	13.4	89.3	1809	12	ADO07771	Ado07771 Human pol

ALIGNMENTS

RESULT 1
AEB28957
ID AEB28957 standard; DNA; 15 BP.
XX
AC AEB28957;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human MCOLN1 gene PCR primer IVS-F SEQ ID NO:1.
XX
KW mucolipidosis IV; high throughput screening; mucolipin-1; MCOLN1; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN US2005153300-A1.
XX
PD 14-JUL-2005.
XX
PF 09-JAN-2004; 2004US-00754446.
XX
PR 09-JAN-2004; 2004US-00754446.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Sun W, Hantash F;
XX
DR WPI; 2005-521160/53.
XX
PT Diagnosing mucolipidosis (ML) IV mutant sequence in nucleic acids, by
PT amplifying the nucleic acid, detecting amplified product with labeled
PT oligonucleotide probes via a change in fluorescence which indicates the
PT presence of an ML IV mutant.
XX
PS Claim 1; SEQ ID NO 1; 15pp; English.
XX
CC The invention relates to a method (M1) for detecting the presence of
CC mucolipidosis IV (ML IV) mutant sequences in a nucleic acid. (M1)
CC involves contacting the nucleic acid with oligonucleotide primers and
CC probes, conducting amplification by temperature cycling and monitoring
CC the accumulation of amplified nucleic acid by detecting an increase in
CC donor fluorophore fluorescence or decrease in acceptor fluorophore

CC fluorescence, which indicates the presence of ML IV mutant sequence. Also
CC described: (1) an oligonucleotide (ON1) comprising a sequence
CC complementary to the coding or non-coding strand of the mucolipin-1
CC (MCOLN1) gene; and (2) a kit (K1) for amplifying sequences of ML IV
CC sequences, comprising ON1. (M1) is useful for determining the presence of
CC ML IV mutant sequence in a nucleic acid, and/or wild-type sequences. (M1)
CC is useful for genetic counseling of individuals at risk for ML IV or at
CC risk to having offspring afflicted with ML IV. The MCOLN1 gene is located
CC on chromosome 19p13. The present sequence represents a PCR primer for the
CC MCOLN1 gene, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 15 BP; 3 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCGGGCCGGACTCA 15
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Db 1 AGCGGGCCGGACTCA 15

RESULT 2
AAK73827
ID AAK73827 standard; DNA; 11365 BP.
XX
AC AAK73827;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
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PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
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PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:41:33 ; Search time 362.28 Seconds
(without alignments)
342.389 Million cell updates/sec

Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	15	100.0	356	8	US-10-425-115-103385	Sequence 103385,
	3	15	100.0	13270	3	US-09-851-494B-1	Sequence 1, Appli
c	4	14	93.3	201	8	US-10-719-993-29684	Sequence 29684, A
	5	14	93.3	432	7	US-10-430-201-1048	Sequence 1048, Ap
	6	14	93.3	432	7	US-10-430-201-1049	Sequence 1049, Ap
c	7	14	93.3	527	5	US-10-027-632-130943	Sequence 130943,
c	8	14	93.3	527	5	US-10-027-632-130944	Sequence 130944,
c	9	14	93.3	527	6	US-10-027-632-130943	Sequence 130943,
c	10	14	93.3	527	6	US-10-027-632-130944	Sequence 130944,
	11	14	93.3	606	7	US-10-767-701-524	Sequence 524, App
c	12	14	93.3	837	6	US-10-369-493-37513	Sequence 37513, A
	13	14	93.3	858	8	US-10-425-115-162360	Sequence 162360,
c	14	14	93.3	4102	8	US-10-602-494-17	Sequence 17, Appl
c	15	14	93.3	19265	8	US-10-719-993-6839	Sequence 6839, Ap
c	16	13.4	89.3	63	7	US-10-362-906-3	Sequence 3, Appli
	17	13.4	89.3	252	6	US-10-029-386-26242	Sequence 26242, A
	18	13.4	89.3	303	3	US-09-974-300-5829	Sequence 5829, Ap
c	19	13.4	89.3	329	8	US-10-425-115-122740	Sequence 122740,
c	20	13.4	89.3	399	9	US-10-779-543-12575	Sequence 12575, A
c	21	13.4	89.3	438	7	US-10-437-963-5136	Sequence 5136, Ap
c	22	13.4	89.3	449	8	US-10-425-115-29829	Sequence 29829, A
c	23	13.4	89.3	483	4	US-09-925-065A-755757	Sequence 755757,
c	24	13.4	89.3	499	4	US-09-925-065A-762110	Sequence 762110,
	25	13.4	89.3	556	6	US-10-029-386-12542	Sequence 12542, A
c	26	13.4	89.3	610	5	US-10-027-632-99325	Sequence 99325, A
c	27	13.4	89.3	610	6	US-10-027-632-99325	Sequence 99325, A
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	29	13.4	89.3	638	8	US-10-425-115-140595	Sequence 140595,
	30	13.4	89.3	645	5	US-10-027-632-28813	Sequence 28813, A
	31	13.4	89.3	645	5	US-10-027-632-28814	Sequence 28814, A
	32	13.4	89.3	645	6	US-10-027-632-28813	Sequence 28813, A
	33	13.4	89.3	645	6	US-10-027-632-28814	Sequence 28814, A
	34	13.4	89.3	648	6	US-10-369-493-39498	Sequence 39498, A
	35	13.4	89.3	648	6	US-10-369-493-39877	Sequence 39877, A
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	37	13.4	89.3	681	5	US-10-001-883-38	Sequence 38, Appl
	38	13.4	89.3	861	6	US-10-156-761-2634	Sequence 2634, Ap
	39	13.4	89.3	968	8	US-10-653-047-7533	Sequence 7533, Ap
	40	13.4	89.3	984	6	US-10-156-761-1305	Sequence 1305, Ap
c	41	13.4	89.3	1052	9	US-10-450-763-20158	Sequence 20158, A
c	42	13.4	89.3	1152	6	US-10-369-493-46700	Sequence 46700, A
	43	13.4	89.3	1353	6	US-10-156-761-4728	Sequence 4728, Ap
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ALIGNMENTS

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; Sequence 1, Application US/10754446
; Publication No. US20050153300A1
; GENERAL INFORMATION:
; APPLICANT: SUN, WEIMIN
; APPLICANT: HANTASH, FERAS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF
; TITLE OF INVENTION: MUCOLIPIDOSIS IV MUTATIONS
; FILE REFERENCE: 034827-2301
; CURRENT APPLICATION NUMBER: US/10/754,446
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-754-446-1

Query Match 100.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCGGGCCGGACTCA 15

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; Sequence 103385, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326

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;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(356)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_25792C.1
US-10-425-115-103385

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Db        255 AGCGGGCCGGACTCA 269


RESULT 3
US-09-851-494B-1
; Sequence 1, Application US/09851494B
; Publication No. US20030064363A1
; GENERAL INFORMATION:
;  APPLICANT: ML4 Foundation
;  APPLICANT:  Goldin, Ehud
;  APPLICANT:  Slaugenhaupt, Susan A.
;  APPLICANT:  Sun, Mei
;  APPLICANT:  Acierno, James S.
;  TITLE OF INVENTION: A Gene Encoding A New TRP Channel is Mutated in Mucolipidosis IV
;  FILE REFERENCE: 3394/1H557US1
;  CURRENT APPLICATION NUMBER: US/09/851,494B
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 13270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-494B-1

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Db       5495 AGCGGGCCGGACTCA 5509


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US-10-719-993-29684/c
; Sequence 29684, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001496
;  CURRENT APPLICATION NUMBER: US/10/719,993
;  CURRENT FILING DATE:  2003-11-24
;  NUMBER OF SEQ ID NOS: 55342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29684
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-719-993-29684

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; Sequence 1048, Application US/10430201
; Publication No. US20040162679A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Linheng
;  TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
;  FILE REFERENCE: 40716 (IP-010)
;  CURRENT APPLICATION NUMBER: US/10/430,201
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: US 60/370,114
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 4879
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1048
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;   ORGANISM: Mus musculus
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;   NAME/KEY: misc_feature
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;   LOCATION: (355)..(355)
;   OTHER INFORMATION: n is a, c, g, or t
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GenCore version 5.1.6

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(without alignments)
65.779 Million cell updates/sec

Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	13.4	89.3	182314	7	US-11-112-908-45	Sequence 45, Appl
	4	13	86.7	1321	6	US-10-750-185-49780	Sequence 49780, A
	5	13	86.7	1321	6	US-10-750-623-49780	Sequence 49780, A
	6	13	86.7	15876	7	US-11-052-554A-660	Sequence 660, App
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c	8	12.4	82.7	65	6	US-10-310-914A-8862	Sequence 8862, Ap
	9	12.4	82.7	126	6	US-10-467-657-867	Sequence 867, App
	10	12.4	82.7	153	6	US-10-467-657-735	Sequence 735, App
	11	12.4	82.7	162	6	US-10-467-657-743	Sequence 743, App
c	12	12.4	82.7	201	6	US-10-995-561-11825	Sequence 11825, A
c	13	12.4	82.7	201	6	US-10-995-561-61260	Sequence 61260, A
c	14	12.4	82.7	201	6	US-10-995-561-82266	Sequence 82266, A
c	15	12.4	82.7	558	7	US-11-212-443-49	Sequence 49, Appl
c	16	12.4	82.7	600	6	US-10-750-185-21924	Sequence 21924, A
c	17	12.4	82.7	600	6	US-10-750-623-21924	Sequence 21924, A
c	18	12.4	82.7	600	7	US-11-136-527-6844	Sequence 6844, Ap
c	19	12.4	82.7	639	7	US-11-212-443-47	Sequence 47, Appl
c	20	12.4	82.7	660	7	US-11-212-443-45	Sequence 45, Appl
c	21	12.4	82.7	696	6	US-10-467-657-3351	Sequence 3351, Ap
	22	12.4	82.7	960	6	US-10-750-185-63567	Sequence 63567, A
	23	12.4	82.7	960	6	US-10-750-623-63567	Sequence 63567, A
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c	25	12.4	82.7	999	6	US-10-750-623-53582	Sequence 53582, A
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c	29	12.4	82.7	1465	6	US-10-750-623-62827	Sequence 62827, A
c	30	12.4	82.7	1581	6	US-10-750-185-64370	Sequence 64370, A
c	31	12.4	82.7	1581	6	US-10-750-623-64370	Sequence 64370, A
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c	33	12.4	82.7	1604	7	US-11-193-715-7	Sequence 7, Appli
c	34	12.4	82.7	1713	7	US-11-136-527-2748	Sequence 2748, Ap
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	36	12.4	82.7	1938	6	US-10-967-527A-29	Sequence 29, Appl
	37	12.4	82.7	1979	6	US-10-967-527A-31	Sequence 31, Appl
	38	12.4	82.7	2232	6	US-10-986-501-79	Sequence 79, Appl
	39	12.4	82.7	2879	7	US-11-124-368A-166	Sequence 166, App
	40	12.4	82.7	3635	7	US-11-136-527-2101	Sequence 2101, Ap
	41	12.4	82.7	4734	7	US-11-136-527-2518	Sequence 2518, Ap
c	42	12.4	82.7	5498	7	US-11-192-967-1	Sequence 1, Appli
c	43	12.4	82.7	5498	7	US-11-193-715-1	Sequence 1, Appli
c	44	12.4	82.7	6719	6	US-10-995-561-456	Sequence 456, App
	45	12.4	82.7	9903	7	US-11-052-554A-517	Sequence 517, App

ALIGNMENTS

RESULT 1
US-10-310-914A-1387400
; Sequence 1387400, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1387400
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1387400

Query Match 89.3%; Score 13.4; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db          2 AGCGGGCUGGACUCA 16
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 654079
; LENGTH: 25

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;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-654079

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RESULT 3
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; Sequence 45, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
;   LENGTH: 182314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-45

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RESULT 4
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49780
;   LENGTH: 1321
;   TYPE: DNA
;   ORGANISM: Bovine  19866880919793
US-10-750-185-49780

  Query Match             86.7%;  Score 13;  DB 6;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
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RESULT 5
US-10-750-623-49780
; Sequence 49780, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-1
;  CURRENT APPLICATION NUMBER: US/10/750,623
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49780
;   LENGTH: 1321
;   TYPE: DNA
;   ORGANISM: Bovine  19866880919793
US-10-750-623-49780

  Query Match             86.7%;  Score 13;  DB 6;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCGGGCCGGACT 13
              |||||||||||||
Db        169 AGCGGGCCGGACT 181


RESULT 6
US-11-052-554A-660
; Sequence 660, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
;  APPLICANT: Sachdeva, et al.
;  TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
;  TITLE OF INVENTION:  PROTEINS OF THERAPEUTIC POTENTIAL
;  FILE REFERENCE: 30853/40359A
;  CURRENT APPLICATION NUMBER: US/11/052,554A
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: US 60/589,227
;  PRIOR FILING DATE: 2004-07-20
;  PRIOR APPLICATION NUMBER: IN 173/DEL/2004
;  PRIOR FILING DATE: 2004-02-06
;  NUMBER OF SEQ ID NOS: 763
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 660
;   LENGTH: 15876
;   TYPE: DNA
;   ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-660

  Query Match             86.7%;  Score 13;  DB 7;  Length 15876;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 16:32:47 ; Search time 54.6 Seconds
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Title: US-10-754-446-1
Perfect score: 15
Sequence: 1 agcgggccggactca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	14	93.3	1950	3	US-09-902-540-3982	Sequence 3982, Ap
c	3	14	93.3	10236	3	US-09-949-016-12492	Sequence 12492, A
c	4	14	93.3	10237	3	US-09-949-016-13859	Sequence 13859, A
c	5	14	93.3	20232	3	US-09-902-540-1197	Sequence 1197, Ap
	6	13.4	89.3	97	3	US-09-513-999C-21303	Sequence 21303, A
c	7	13.4	89.3	616	3	US-09-533-559-599	Sequence 599, App
	8	13.4	89.3	968	3	US-09-533-559-7533	Sequence 7533, Ap
c	9	13.4	89.3	981	3	US-09-489-039A-99	Sequence 99, Appl
	10	13.4	89.3	1281	3	US-09-489-039A-6674	Sequence 6674, Ap
	11	13.4	89.3	2301	2	US-08-614-801A-5	Sequence 5, Appli
c	12	13.4	89.3	2524	3	US-10-104-047-517	Sequence 517, App
c	13	13.4	89.3	2868	3	US-09-543-681A-1961	Sequence 1961, Ap
c	14	13.4	89.3	2874	3	US-10-104-047-1915	Sequence 1915, Ap
	15	13.4	89.3	3048	3	US-09-023-655-957	Sequence 957, App
c	16	13.4	89.3	3292	2	US-08-611-107-33	Sequence 33, Appl
	17	13.4	89.3	3882	3	US-09-252-991A-1005	Sequence 1005, Ap
c	18	13.4	89.3	4404	3	US-09-252-991A-1086	Sequence 1086, Ap
	19	13.4	89.3	42276	3	US-09-949-016-17218	Sequence 17218, A
c	20	13	86.7	387	3	US-09-280-116-41	Sequence 41, Appl
	21	13	86.7	444	3	US-09-252-991A-11937	Sequence 11937, A
	22	13	86.7	471	3	US-09-252-991A-8611	Sequence 8611, Ap
	23	13	86.7	696	3	US-09-252-991A-11970	Sequence 11970, A
	24	13	86.7	732	3	US-09-252-991A-11900	Sequence 11900, A
	25	13	86.7	975	3	US-10-152-886-98	Sequence 98, Appl
c	26	13	86.7	1119	3	US-09-252-991A-12015	Sequence 12015, A
c	27	13	86.7	2214	2	US-07-985-458-1	Sequence 1, Appli
	28	13	86.7	4162	3	US-09-453-702B-259	Sequence 259, App
	29	13	86.7	4162	3	US-10-114-170-259	Sequence 259, App
c	30	13	86.7	4382	3	US-09-949-016-15098	Sequence 15098, A
	31	13	86.7	25165	3	US-09-453-702B-39	Sequence 39, Appl
	32	13	86.7	25165	3	US-10-114-170-39	Sequence 39, Appl
c	33	13	86.7	35471	3	US-09-949-016-12957	Sequence 12957, A
c	34	13	86.7	41522	3	US-09-949-016-11932	Sequence 11932, A
c	35	13	86.7	41523	3	US-09-949-016-15764	Sequence 15764, A
	36	13	86.7	58857	3	US-09-477-962-1	Sequence 1, Appli
	37	12.4	82.7	24	3	US-09-507-819-1	Sequence 1, Appli
	38	12.4	82.7	24	3	US-09-507-819-69	Sequence 69, Appl
	39	12.4	82.7	24	3	US-09-507-819-70	Sequence 70, Appl
	40	12.4	82.7	24	3	US-09-641-576-1	Sequence 1, Appli
	41	12.4	82.7	24	3	US-09-641-576-69	Sequence 69, Appl
	42	12.4	82.7	24	3	US-09-641-576-70	Sequence 70, Appl
	43	12.4	82.7	96	3	US-09-507-819-33	Sequence 33, Appl
	44	12.4	82.7	96	3	US-09-507-819-35	Sequence 35, Appl
	45	12.4	82.7	96	3	US-09-507-819-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-13454
; Sequence 13454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13454
; LENGTH: 15353
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13454

Query Match 100.0%; Score 15; DB 3; Length 15353;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCGGGCCGGACTCA 15
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Db       6095 AGCGGGCCGGACTCA 6109
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RESULT 2
US-09-902-540-3982/c
; Sequence 3982, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10

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;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3982
;    LENGTH: 1950
;    TYPE: DNA
;    ORGANISM: Myxococcus xanthus
US-09-902-540-3982

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  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
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Db        608 AGCGGGCCGGACTC 595


RESULT 3
US-09-949-016-12492/c
; Sequence 12492, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12492
;    LENGTH: 10236
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12492

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGGGCCGGACTCA 15
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Db       2595 GCGGGCCGGACTCA 2582


RESULT 4
US-09-949-016-13859/c
; Sequence 13859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13859
;    LENGTH: 10237
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-13859

  Query Match             93.3%;  Score 14;  DB 3;  Length 10237;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGGGCCGGACTCA 15
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Db       2595 GCGGGCCGGACTCA 2582


RESULT 5
US-09-902-540-1197/c
; Sequence 1197, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1197
;    LENGTH: 20232
;    TYPE: DNA
;    ORGANISM: Myxococcus xanthus
;    FEATURE:
;    NAME/KEY: unsure
;    LOCATION: (1)..(20232)
;    OTHER INFORMATION: unsure at all n locations
US-09-902-540-1197

  Query Match             93.3%;  Score 14;  DB 3;  Length 20232;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      18886 AGCGGGCCGGACTC 18873


RESULT 6
US-09-513-999C-21303
; Sequence 21303, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 21303
;    LENGTH: 97
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-513-999C-21303

  Query Match             89.3%;  Score 13.4;  DB 3;  Length 97;
  Best Local Similarity   93.3%;  Pred. No. 9.5e+02;
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